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AF421380 Homo sapi

AF279145 Homo sapi

BC012074 Homo sapi

AK001463 Homo sapi

AK001463 Homo sapi

AK001403 Homo sapi

AK001405 Homo sapi

AK002160 Homo sapi

AK002171 Homo sapi

AK110155 Homo sapi

AK120151 Homo sapi

AK143871 Homo sapi

AK13871 Homo sapi

AK1387059 Human Chr

AK10518 Homo sapi

AK145038 Human DNA

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AC01754 Homo sapi

AC008738 Homo sapi

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HOmo Saprens anthrax toxin receptor mRNA, complete cds.
AF421380
AF421380.1 GI:16566412
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2 (bases 1 to 1414)
Bradley,K.A., Mogridge,J., Mourez,M., Collier,R.J. and Young,J.A.T.
Direct Submission
Submitted (19-SEP-2001) Department of Oncology, University of
Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA
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1 (bases 1 to 1414)
Bradley,K.A., Mogridge,J., Mourez,M., Collier,R.J. and Young,J.A.T.. Identification of the cellular receptor for anthrax toxin Mature 414 (6860), 225-229 (2001)
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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St. Croix,B., Vogelstein,B. and Kinzler,K.W.
Direct Submission
Direct Submission
Submitted (16-JUN-2000) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA B (bases 1 to 5540)
S St. Croix,B., Vogelstein,B. and Kinzler,K.W.
Direct Submission
L Submitted (09-MAY-2001) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA Sequence update by submitter
On May 9, 2001 this sequence version replaced gi:9857405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 5540)
St. Croix,B., Rago,C., Velculescu,V., Traverso,G., Romans,K.E., Montgomery,E., Lal,A., Riggins,G.J., Lengauer,C., Vogelstein,B. Rinzler,K.W.
                                                                                                                                                                                                           tecatectggccategecetgetgatectgttectgetectagecetggetetectetgg 1020
                                                                                                                                                                                                                                                      Homo sapiens tumor endothelial marker 8 precursor (TEM8) mRNA, complete cds.
AF279145.2 GI:14017380
                                                                          1064 TCCATCCTGGCCATCGCTGCTGATCCTGTTCCTGCTCCTAGCCCTGGCTCTCTTTGG
                                Genes expressed in human tumor endothelium Science 289 (5482), 1197-1202 (2000)
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Matches 1104; Conservative 0; Mismatches
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ALLAMWFWPLCCTYTIKEVGWRAALGYSMNGANGFRFPPREDDDGLPKKKRMFTVDSYTGRGVGGTH
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                                                                                                                                 KGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPP
APIYTPPPPAPHCPPPPPSAPTPPIPSPSTLPPPPQAPPDNRAPPPSRPPPRSV"
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1104. :1172
/gene="TEM8"
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Pred. No. 0;
0; Mismatches
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1187 g 1446 t
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Best Local Similarity 99.8%;
Matches 1092; Conservative
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PRI 06-AUG-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2112)
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Submitted (02-AUG-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    840
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720
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                                                                                         atcgaaattctagcagctgaaccatccaccatatgtgcaggagagtcatttcaagttgtc
                          atcaatgactcggtcacactcaatgagaagcccttttctgtggaagacacttatttactg
                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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BC012074.1 GI:15082332
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 5220)
Carson-Walter,E.B., Watkins,D.N., Nanda,A., Vogelstein,B., Kinzler,K.W. and St. Croix.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carson-Walter, E.B., Vogelstein, B., Kinzler, K.W. and St. Croix, B. Direct Submission
Submitted (10-May-2001) Oncology, Johns Hopkins University, 1650
Orleans Street, Baltimore, MD 21231, USA
Location/Qualifiers
                                                                                                                                                                             1012
                                                                                        892
                                                                                                            840
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                                                                                                                                                                                                                                                              5220 bp mRNA linear ROD 07-OCT Mus musculus tumor endothelial marker 8 precursor (Tem8) mRNA, ocmplete cds.
GIGAAIGACGGCITICAGGCICIGCAAGGCAICCACCCAAITIIGAAGAAGICCIGC 772
                                                                                                                                                       atcaatgactcggtcacactcaatgagaagccctttctgtggaagacacttattactg
                                   atcgaaattctagcagctgaaccatccaccatatgtgcaggagagtcatttcaagttgtc
                                                                                                                         Res. 61 (18), 6649-6655 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
1. .5220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274. .1962
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274. .1962
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KEYWORDS
SOURCE
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JOURNAL
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    Series: IRAL Plate: 29 Row: g Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7022737.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                             Length 2112;
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Pred. No. 2.4e-276;
0; Mismatches 1;
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ilarity 99.9%;
Conservative
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VYRGNGFRHARNVDRVLCSFKINDSVTLSKŠLOSPWVSSTSGFKEGNSHPCLPARPHT
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                                                                                                              1043
                                                                                                                gatcctgttcctgctcctagccctggctctcctctggtggttctggccctctgctgcac
                         ttctgtcatcatcaccaccacactgttctgacggttccatcctggccatcgccttgct
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                    /cell_type="teratocarcinoma"
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/note="cloning vector: pME18SFL3; mRNA from Precursor cells after 2-weeks retinoic acid (Induction.")
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Homo sapiens cDNA FLJ10601 fis, clone NT2RP2005000.
AK001463
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Homo sapiens teratocarcinoma cell_line:NT2
clone_lib:NT2RP2 clone:NT2RP2005000.
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/db_xref="G1:7022738"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP2005000"
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/note="unnamed protein
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Pred. No. 4e-247;
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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T. Tanaka, T. and Nakamura, Y. Shibahara, T. Tanaka, T. and Naka, T. and Naka, T. and Naka, Submitted (29-Aug. 2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5' & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
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Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tamaka, T., Nakamura, Y., Isogai, T. and Sugano, S. Unpublished (2000)
2. (bases I to 4007)
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Pred. No. 6.2e-153;
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/db_xref="GI:10437939"
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/db_xref="taxon:9606"
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/cell_line="Hep62"
/cell_type="heptoma"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
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Homo sapiens cDNA: FLJ21776 fis, clone HEP00171.
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Homo sapiens hepatoma cell_line:HepG2 cDNA
clone:HEPG0171.
Homo sapiens
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                                         ed. No. 4e-227;
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                                               98.38;
                                               Similarity 99.3
                                               Best Local
Matches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics Laboratory; 153-23 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NBDO buman cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- 6 3'-end one pass sequencing: RAB, HRI, and Blotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
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Shibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
Kusano,J., Watanabe,M., Fuljimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T., Sugano,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
                                                                                                                  ggcaagggggacgcagggaggatggggtccagcctgctacggcggatttgacctgtact 139
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Homo sapiens CDNA FLJ32754 fis, clone TESTI2001671.
AK057316
                                                                                                                                                                                                                                                                                                                       insert sequence).
to mRNA, clone_lib:TESTI2
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Pred. No. 6.1e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="TESTI2001671"
/tissue_type="testis"
/clone_lib="TESTI2"
/note="cloning vector: pi
a 614 c 517 g 45
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1. .2126
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Homo sapiens testis cDNA
clone:TESTI2001671.
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56.6%;
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PRI 20-AUG-2001
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Bukaryotas; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 1297)
Strausberg, R.
Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
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                                                                                                                           CAGACGGCCAGACTGTCTTGCCACTCACCTCAGACAAGAATAGAATAAAAAACGGTCTTG
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aacagttggctcacaaattcatcagcccacagttgagaatgtcctttattgttttctcca
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/translation="MRLSFTYESSOATILPLTGDRGKISKGLEDLKRVSPVGETYIH
EGLKLANBQIOKAGGLKTSSIIIALTDGKLDGLVPSYAEKERKISKGLASYVCVGVL
BEDQACLERTADSKEOVFPVKGGFQALKGIINSILAGSCTEILELQPSSVCYGEEFQI
VLSGRGFMLGSRNGSVLCTYTVNETYTSVKPVSVQLNSMLCPAPILNKAGEWGLTVT
QAGVKWHDLTHCTFGLSGSGDPPTSAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-07-2001) Takao Isogai, Helix Research Institute, Submitted (24-07-201) Takao Isogai, Helix Research Institute, Cahonaics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) Rubo human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library of construction: Helix Research Institute (HRI) (supported by Japan Kry Technology Center etc.); 5'-6', 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                                                                       Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Ninomiya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Kamihara, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S.,
Yamamoto, J., Isono, Y., Kawai-Hoo, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fuji, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.,
NEDO human cDNA sequencing project
   oligo capping; fis (full insert sequence).

Homo sapiens synoviceytes from rtheumaticid arthritis (HS-RA) cDNA to mRNA, clone_lib:HSYRA2 clone:HSYRA2001476.

Homo sapiens
                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="synoviocytes from rtheumatiold arthritis
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ilarity 59.9%; Pred. No. 8.7e-59;
Conservative 0; Mismatches 268;
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/protein_id="BAB70976.1"
/db_xref="GI:16550415"
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/db_xref="taxon:9606"
/clone="HSYRA2001476"
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                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                       REFERENCE
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VERSION
KEYWORDS
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/codoi_start=2
/product="Unknown (protein for IMAGE:4705862)"
/product="Unknown (protein for IMAGE:4705862)"
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/db_yref="GT:15246848484"
/db_yref="GT:1524684848484"
/db_yref="GT:
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                                                                                                                                                                                                                                                                                                   Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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0
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/db_xref="taxon:9606"
/clone="IMAGE:4705862"
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/lab_host="NHH_MGC_87"
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Homo sapiens cDNA FLJ31074 fis, clone HSYRA2001476
AK055636
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Pred. No. 5.5e-60;
0; Mismatches 5; Indels
                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV-SPORT6"
                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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LYFVLDKSGSVANNWIEIYNFVQQLAERFVSPEMRLSFIVFSSQATIILPLTGDRGKI
SKGLEDLKYNSPVGEYYIHECLKLAMPOLOKAGCKTKSSLITALTDGALDSVPSAE
SKGLEDLKYNSPVGEYYIHECLKLAMPOLOKAGCKTSSLITALTDGALGINSSYAE
KEAKI SKSLGASVYCVGVLDPEQAGLERIADSKEQVFPVKGGFQALKGIINSSNGIAA
IIVILVLLLLGIGLMWWFWPLCCKVVIKDPPPPPPAPAFKEEEEEPLPTKKWPTVDAS
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297 c 377 g 326 L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tcagagaggaggctaataggtctcgagatcttggtgcaattgtttactgtgtttggtgtg
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Oligo capping; fis (full insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1009794.
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Pred. No. 2e-
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(Dases 1 to 1343)

Bell,S.E., Mavila,A., Salazar,R., Bayless,K.J., Kanagala,S., Maxwell,S.A. and Davis,G.E.
Maxwell,S.A. and Davis,G.E.
obliferential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling
J. Cell. Sci. 114 (Pt 15), 2755-2773 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 22-JAN-2002
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AY040326.1 GI:15418998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="CMG-2; contains a von Willebrand factor A domain; regulated during endothelial cell morphogenesis; targets to the endoplasmic reticulum"
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Submitted (14-JUN-2001) Pathology, Texas A&M University System
Health Science Center, 208 Reynolds Medical Building, College
Station, TX 77843-1114, USA
Location/Qualifiers
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ggatttgaaagggccagtgagcagatttattatgaaaacagacaagggtacaggacagcc
                          GGACTAAAGCTAGCGAATGAACAAAT-----TCAGAAAGCAGGAGGCTTGAAAACCTCC
                                                         agcgicalicatificatitigacigatigagagacticatigaagaticitititititaticagag
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/db_xref="taxon:9606"
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/organism="Homo
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141. .1301
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Davis, G.E. and Bell, S.E.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 7 Row: e Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579 g
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Similarity 57.6%;
56; Conservative (
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Isogal, T. and Otsuki, T.

Direct Submission

Direct Submission

Submitted (16-FEB-2000) to the DDBJ/EWBL/GenBank databases. Takao

Submitted (16-FEB-2000), To the DDBJ/EWBL/GenBank databases. Takao

Isogal, Helix Research Institute, Genomics Laboratory; 1532-3 Yana,

Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,

Tel:81-8438-52-3951, Fax:81-438-55-3952)

NEDO human CDNA sequencing project supported by Ministry of

International Trade and Industry of Japan, CDNA full insert

International Trade and Industry of Japan, CDNA full insert

Sequencing: Research Association for Biotechnology; CDNA library

construction, 5- & 3'-end one pass sequencing and clone selection:

Helix Research Institute (supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science,

University of Tokyo.
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Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                        Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Naqai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugwawara, Takfahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Sugwawara, M., Takfauchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nachuman cDNA sequencing project (Inpublished (2000)
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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307 t
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Mus musculus, clone IMAGE:3484366, mRNA,
BC003908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1009794"
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/note="cloning_vector: }
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AC025010 81017 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                           TATECTNGIAAIVAILVLLLLGAALMWWFWPLCCKVVIKDPPPPPSRPMEEEEEDPL
PNKKWPTVDASYYGGRGVGGIKRMEVRWGDKGSTEEGARLEKAKNAVYWVPEEEIPIP
SRPPRPRPTHQAPQTKWYTPIKGRLDALWALIMKQYDRVSLMRPQEGDEGRCINFSRV
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0
                                                                                                                                                                                                                    /product="Unknown (protein for IMAGE:3484366)"
/protein_id="AAH03908.1"
/db_xref="G1:13278124"
/translation="EKPVSIQPSSILCPAPVLNKDGETLEVSISYNDGKSAVSRSLTI
                                                              /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92.8; DB 10;
Pred. No. 1.8e-16;
0; Mismatches 122;
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                                                                                                                                                             /note="Vector: pcmv-sPORT6"
                                                                                              old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                   670
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3484366"
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43 19742: Gontig of 75 bp in length 20493: contig of 751 bp in length 24 20593: contig of 751 bp in length 24 20593: contig of 744 bp in length 100 bp 22202: contig of 765 bp in length 100 bp 22302: contig of 765 bp in length 100 bp 23072: contig of 769 bp in length 100 bp 23073: contig of 769 bp in length 100 bp 24 2041: gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 
                                                                                                                                                                                                                                                                                             88 12857; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp
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: contig of 785 bp ii
ap of 100 bp
: contig of 776 bp ii
                                               8567: gap of 100 bp
9320: contig of 753 bp
9420: gap of 100 bp
10187: contig of 767 bp
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29969: contig of 765 bp
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contig of 768 bp
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32576: contig of 766 bp
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38676: contig of 761 bp
38776: gap of 100 bp
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14494 14593: gap of
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31710: cont
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111143 11910: cont.
11911 12010: gap of
12011 12757: cont.
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5449 16206: con
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                                         /: gap of
9320: con
     : gap
8467:
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                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 81017)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This record contains 94 individual

* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
of 766 bp in length
100 bp
of 760 bp in length
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contig of 777 bp in length
                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-85D17
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: 85_D_17
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4176: con
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5036: con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
                                                                                                                                                                                                  (bases 1 to 81017)
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                       Homo sapiens
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SOURCE
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unpunished
2 (bases 1 to 81017)
2 (bases 1 to 81017)
2 (bases 1 to 81017)
3 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Barna, N., Bastlan, V., Baeda, F., Anderson, S., Baldwin, J., Barown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Colge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Rarata, J., Lakogue, K., Johnson, R., Jones, C., Kann, L., Karatas, A., Hein, J., Lakogue, M., Lamazares, R., Landers, T., Lehoczky, J., Kalin, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
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Homo sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                           Austrinstied, GERMANY
Clone from S. Wiemmann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemmann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemmann, Molecular Genome Analysis, German Cancer
Cherz, Fessearch Center (DRFZ); Email S. Wiemmann, Within the CDNA sequencing
consortium of the German Genome Project.
This clone (DRFZ)56F1349 is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
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1 (bases 1 to 81017)
Birran, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-85D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2586F1324"
/clone=lib="586 (synonym: hutel). Vector pSportl; host
/clone=lib="566"
/clone=lib="566"
/clone=lib="566"
/clone=lib="566"
/clone=lib="566"
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Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
                                                                                                                              Submitted (15-AUG-1999) MIPS, Am Klopferspitz 18a, D-82152
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Pred. No. 0.0064;
0; Mismatches 15; Indels
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1840. .1845
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AC025010.1 GI:7145054
HTG; HTGS_PHASE0.
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Matches 57; Conservative
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                                                                                 Wiemann,S.
Direct Submission
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KEYWORDS
SOURCE
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Homo sapiens mRNA; cDNA DKFZp586F1324 (from clone DKFZp586F1324).
AL110155
AL110155.1 GI:5817057
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                        17 41416: gap of 4.1517 by 11. Long of 4.15181: contig of 765 bp in length 4.2181: contig of 765 bp in length 18.2 42381: gap of 100 bp 13.3 43130: gap of 100 bp 100 bp 13.3 43130: gap of 100 bp 14.4770: contig of 783 bp in length 4.4770: contig of 783 bp in length 18.3 1 43531: contig of 783 bp in length 18.3 1 45631: contig of 781 bp in length 18.3 45631: contig of 781 bp in length 18.3 45631: contig of 783 bp in length 18.3 45687: contig of 783 bp in length 18.4 47340: contig of 783 bp in length 18.4 47340: contig of 783 bp in length 18.4 47340: contig of 783 bp in length 18.5 4528: contig of 783 bp in length 19.2 4528: contig of 783 bp in length 19.2 4528: contig of 787 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 788 bp in length 19.2 49028: contig of 78
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                                                                                                                                  40545: gap of 100 bp 4136: contig of 771 bp in length 41316: contig of 775 bp in length 42181: contig of 765 bp in length
                                                 39663: gap of 100 bp 40445: contig of 782 bp in length
                    in length
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96.1%; Pred. No. 7.6e-10;
Live 0; Mismatches 3;
                            contig of
                                                                                                                                           40446 40545; gap of
40346 41316; conti
41317 41416; gap of
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50748:
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Matches 74; Conservative
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DEFINITION

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73 23172; 949 of 769 bp in length 24041; 949 of 769 bp in length 24041; 949 of 769 bp in length 24041; 949 of 760 bp in length 100 bp 25667; contig of 768 bp in length 100 bp 26515; contig of 768 bp in length 100 bp 26515; contig of 760 bp in length 100 bp 26515; gap of 100 bp 27475; gap of 100 bp 2747
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13 20493: contig of 751 bp ir

14 20593: gap of 100 bp

14 21377: contig of 744 bp ir

18 21437: gap of 100 bp

18 22202: contig of 765 bp ir
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47441 48171: contig of 731 bp
48172 48271: gap of 100 bp
45631: contig of 7
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                            Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Ollvar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Ray. Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Taravers, M., Trigilio, J., Vassiliev, H., Viel, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vangiliev, H., Viel, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vong, G., Zainoun, J., Zimmer, A. and Zody, M.

L. Submitted (03 "AR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using Repeathwsker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 94 individual

* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that

the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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; 0 0; Gaps Query Match

4.3%; Score 48; DB 2; Length 81017;
Best Local Similarity 79.2%; Pred. No. 0.017;
Matches 57; Conservative 0; Mismatches 15; Indels

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Search completed: August 9, 2002, 00:24:29 Job time: 12526 sec

Amino acid sequenc A murine TANGO 216 A murine TANGO 216

AAB18448 AAB18460 AAB18459

Human immune/haema TANGO 197.

Mouse alpha-d s Mouse beta 2 in Mouse alpha-d #

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AAW72835 AAW65102 AAW73346 AAR78168 AAW72836

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AAW65101 AAW60001 AAB07371

AAW73344 AAR78169 **AAR78166**

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Rat alpha-d #1, R Human alpha-d, Ho Human Beta-integri Human; secreted protein; prollferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDselmer; adisease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19. Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94. "Mature human secreted protein" ALIGNMENTS 1..27 /label= Signal_peptide 28. 403 /note= "Mature human se AAW72837 AAW72824 AAW72825 Location/Qualifiers AAE01439 standard; Protein; 403 AA (first entry) Peptide Protein

WO200134626-A1

Human protein sequ A human TANGO 216 Amino acid sequenc A human TANGO 216 A human TANGO 216

AAM38976 AAB92985 AAB18456

AAB18447 AAB18455 AAB18457 AAU19662 AAB18458

Human polypeptide

17-MAY-2001

Human novel extrac A murine TANGO 216

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241 vrgngfrharnvdrvlcsfkindsvtlnekpfsvedtyllcpapilkevgmkaalqvsmn 300
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                                                                                                                                                                                                                                                                                                                    AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01456-AAE01513 represent the proteins they encode. protein genes, and AAE01544 represent human secreted protein for preventing, the grade and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene treating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions can be diagnosed by determining the mown protein in a sample or by determining the presence of amount of the new genes. Specific uses are described for each of the mutations in the new genes in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental conditions and include developing products for the diagnosis or treatment of proliferative disorders, diseases of the immune system, allergies, neurological disorders, diseases of the immune system, allergies, neurological disorders (e.g., Alzheimer's diseases).

Callorinestinal disorders, pregnancy-related disorders, and infections. The proference and also be used to aid wound disorders, and infections. The profileration, for supporting celluring and epithelial cell proliferation, for supporting culture of primary tissues, to regenerate tissues, to identify their culture of primary tissues, to regenerate tissues, to identify their contract of primary tissues, to regenerate tissues, to identify their contracting symptoms associated with the disorders mentioned above, and immunosorbent assay (ELISA). The present sequence represents a human corrected protein of the invention.
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                                                                                                                                                                                                                       New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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                                                                                                                                                                                                                                                                                                  Claim 11; Page 485-486; 562pp; English.
                                                                                                                                            Ruben SM, Komatsoulis GA, Moore PA,
                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                           05-NOV-1999; 99US-0163581.
30-JUN-2000; 2000US-0215133.
                           01-NOV-2000; 2000WO-US30045.
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Best Local Similarity
                                                                                                                                                                                 WPI; 2001-308778/32.
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New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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DGLSFISSSVIITTTHCSDGSILAIALLILELLIALALLWWFWPLCCTVIIKEVPPPPAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
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/label= Signal_peptide
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/note= "Encoded by
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/note= "Encoded
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30-JUN-2000; 2000US-0215133.
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001
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                                                                                                                  361 ESE 363
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(first entry)
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Matches 318; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA47455.
                                                             Human TANGO 197.
                                                                                                                                                                                                                                                                                                                           WO200039284-A1.
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1998;
                       20-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                     06-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                           ANDUSION-AADDS379 represent CDNAS corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental and caveloping products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, ALDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, ALDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, ALDS, autoimmune diseases, (e.g., rheumatoid arthritis), inflammation, ALDS, autoimmune diseases, or proteins (e.g., Alzheimer's disease, cardiovascular disorders, and infections. The proteins can also be used to aid wound disorders, and infections. The proteins can also be used to aid wound the aliands or binding partners, and in chemicals, and infections bending and epithelial cell proliferation, for prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting conturne of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemicals, and anditive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in allewiating symptoms associated with the disorders mentioned above, and immunosorbent assay (ELISA). The present sequence represents a human ever a human ever a human ever a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.7%; Score 1870; DB 22; Length 403; 99.2%; Pred. No. 4.6e-191; ive 0; Mismatches 3; Indels 0
Claim 11; Page 505-506; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB01422 standard; Protein; 333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 AA;
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Matches 360;
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's cliseases e.g. myasthemia gravis, autoimmune diabetes and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEGFERASEOIYYENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
TANGO, 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psofiasis; inflammatory bowel disease; septic shock; ulcerative collitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; chronic myelogenous leukemia; cancer; liver disease; dolfsthis disease; osteoarthritis; lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.5e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.2%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                       prognosis; prophylatic; therapeutic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular disorders can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 4; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                AAB92985;
                                                     Sequence
                                                                                    Query Match
                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide of polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, democtactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                           300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for treating disorders
KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
                                           VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                       Ren F, W
Zhang J;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen R, Ma Y, (
Xu C, Xue AJ,
, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 2121; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useron as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen R,
                                                                                                                                                                       AA.
                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 2121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Asundi V, Ch
Wang 2, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                       AAM38976 standard; Protein; 297
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2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0488725.
2000US-0552317.
2000US-0598042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0727344
                                                                                                       301 dglsfisssviitthcs 318
                                                                                           301 DGLSFISSSVIITTHCS 318
                                                                                                                                                                                                                    (first entry)
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N-PSDB; AAI58132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                 WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 - SEP - 2000;
19 - OCT - 2000;
29 - NOV - 2000;
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25-APR-2000;
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                    22-OCT-2001
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Zhao QA,
                                                                                                                                                                                                                                                                                                                        leukaemia.
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                                                                                                                                                                                               AAM38976;
     181
                                                                                                                                                    RESULT
AAM38976
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                            Note: The sequence data for this patent did not form part of the printed specification.
assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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                                                                                                                                                                                                                                                                                                                                                                                         KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                                                                                                                     HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                              1 MATABRRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
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                                                                                                                                                      Length 297;
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H
                                                                                                                                                                                          Indels
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 11706; 2537pp + CD ROM; English.
                                                                                                                                                        DB 22;
                                                                                                                                                         Score 1392; DB 22;
Pred. No. 4e-140;
2; Mismatches 0;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence SEQ ID NO:11706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 VRGNGFRHARNVDRVLCSFKINDSVTLNE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 vrgngfrharnvdrvlcsfkindsvtlsk 269
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, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB92985 standard; Protein; 218
                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0248036
                                                                                                                                                           72.7%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                Conservative
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                                                                                                                                                                             Best_Local Similarity
Matches 267; Conserv
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence of complementary to a polynucleotide which comprises a 3'-end sequence of complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the edetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs are primers also well and the sexiple of the full-length cDNAs asaily without any specialised methods. AAH13628 and AAH13633 to AAH13632 to AAH13632 to AAH13632 to represent human amino acid sequences; and AAH13632 to AAH13632 to represent chuman amino acid sequences; and AAH13632 to AAH13632 to represent plugonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
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Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -

Fraser CC;

Sharp JD,

Barnes TM, Holtzman DA, WPI; 2000-579269/54.

N-PSDB; AAA75158

(MILL-) MILLENNIUM PHARM INC

01-MAR-2000; 2000WO-US05226.

99US-0122458

01-MAR-1999;

218 AA; Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO 266; TANGO 216;; TANGO 261; TANGO 267;

cellular proliferation; cellular differentiation; cellular adhesion;

von Willebrand factor-associated disorder; cell trafficking; cancer;

hematopoietic associated disease; atelectasis; pulmonary congestion;

oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;

intestinal disorder; spleen associated disease; renal disorder;

cardiovascular disorder; ischemic heart disease; hydrocephalus;

brain herniation; iatrogenic disease; inflammation; meningitis;

Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;

multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                         80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 139
                                                                                                                  RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 199
                                                                                                                                   Gaps
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   Length 218;
                              Indels
Score 966; DB 22;
Pred. No. 9.5e-95;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                        AAB18456 standard; Protein; 488 AA.
 50.5%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-2001 (first entry)
                Best Local Similarity 98.9
Matches 188; Conservative
                                                                                                                                                                                                                                                    260 KINDSVTLNE 269
                                                                                                                                                                                                                                                                                                                                                                     AAB18456;
    Query Match
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WO200052022-A1 Homo sapiens.

08-SEP-2000,

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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cecilular be used to used to omodulate cellular specification, modulate cellular adhesion. The polypeptides can be used to orreat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, understand the bronchiets associated diseases and disorders, spleen associated associated diseases and disorders, spleen associated as schma and bronchiectasis, intestinal disorders, spleen associated as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral cartilade and viral meningitis, Alzheimer's Disease, inflammations, hydrocephalus and encephalitis, and treat hepatic disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disease, multiple sclerosis, brain cancers, context hepatic disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disease, multiple sclerosis, brain cancers, context hepatic disease, multiple specification; it was context and context hepatic disease, multiple specification; it was context and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 175pp; English.
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The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267..The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular allest to treat any von Willebrand
                                                                                                                                                                               equilibries and proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; hematopoietic associated disease; atelectrasis; pulmonary congestion; intestinal disorder; spleen associated disease; renal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; harin herniation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 265, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                 /note= "mature process" /note= "you Willebrand factor A domain" /note= "you Willebrand factor A domain"
                                                                                                                                                                         266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                      Amino acid sequence of human TANGO 216 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "transnmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "extracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                           "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                               "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                      ..488
ote= "mature protein"
                                                                                                                                                                                                                                                                                                                                        /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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                                                                                        AAB18447 standard; Protein; 488 AA.
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                                                                                                                                     (first entry)
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318..341
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98..317
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N-PSDB; AAA75149.
                  359 AEESEE 364
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                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                     15-JAN-2001
                                                                                                                  AAB18447;
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factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative cellular interactions, modulate the proliferation, disorders, such as cancer, modulate the proliferation, differentiation, disorders, such as cancer, modulate the proliferation, differentiation, cells that appear in the bone marrow, and leukocytes, creat bone marrow, blood and hematopoletic associated diseases and chronic bronchits, bronchial asthma and bronchiectasis, intestinal chronic bronchits, bronchial asthma and bronchiectasis, intestinal chronic bronchits, bronchial asthma and bronchiectasis, intestinal cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders astoriated diseases or cells and to treat bone and/or function of bone and cartilage covaries, cerebral ocema, hydrocephalus, brain herniations, iatrogenic covaries, cerebral ocema, hydrocephalus, brain meningitis, Alzheimer's presses, inflammations, bacterial and viral meningitis, and treat hepatic chronics, carebral covaries, parkinson's disease, multiple sclerosis, associated and creat hepatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%; Score 957.5; DB 21;
51.6%; Pred. No. 2.7e-93;
Live 63; Mismatches 107;
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|361 keeeee 366
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Best Local 9
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254 RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT 313

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314 TTHCSDGSILAIALLILFLLALALLWWFWPLCCTVIIKEVPPP----PAEESEE 364

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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 clubar differation, modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to creat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, and late appear in the bone matrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, splean arsociated stream or operation or oedema, emphysema, chronic bronchitis, bronchial stream and bronchiectasis, intestinal disorders, splean associated diseases, modulate trenal disorders, splean associated diseases, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. The patch cancers, created chashed associated does not appear in the specification; it was created with the version of the patch of the core of the core of the core of the core of the present sequence does not appear in the specification; it was created with the version of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the 
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Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser CC;
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Best Local Similarity 52.4<sup>†</sup>
Matches 186; Conservative
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N-PSDB; AAA75157.
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                                                                                                                                                 Homo sapiens.
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; concer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

A human TANGO 216 polypeptide clone.

(first entry)

15-JAN-2001

AAB18457;

AAB18457 standard; Protein; 488 AA

AAB18457

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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO 260 cescribes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, and learn to the bone marrow, and leukocytes, treat bone marrow, and leukocytes, treat bone marrow, and leukocytes, treat bone marrow, and nematopoietic associated diseases and disorders, atelectasis, bulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial astochemic heart disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations,
ENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYY 133
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Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -

Disclosure; Page -; 175pp; English.

Fraser CC;

Sharp JD,

Barnes TM, Holtzman DA,

WPI; 2000-579269/54. N-PSDB; AAA75159.

(MILL-) MILLENNIUM PHARM INC.

99US-0122458.

01-MAR-1999;

01-MAR-2000; 2000WO-US05226.

WO200052022-A1 Homo sapiens

08-SEP-2000.

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3,
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bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders: note: the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                 123 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
                                                                                                                                                                                                             FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
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                                                                                                                                                                                                                                                                                       YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE
                                                                                                                                                                                                                                                 7;
                                                                                     DB 21; Length 488;
                                                                                    Query Match
Best Local Similarity 51.4%; Pred. No. 5.6e-93;
Matches 188; Conservative 64; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human novel extracellular matrix protein, Seq ID No 312.
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2000US-0180628.
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                                                            488 AA;
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04-FEB-2000;
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                                                              Seguence
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08-SEP-2000; 2000US-0231413.

08-SEP-2000; 2000US-0231414.

08-SEP-2000; 2000US-0231414.

08-SEP-2000; 2000US-02328080.

08-SEP-2000; 2000US-02328081.

14-SEP-2000; 2000US-0233998.
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2000US-0234997.
2000US-0234998.
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20000S-0232399.
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20000S-0232401.
20000S-0233063.
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2000US-0233065.
2000US-0234223.
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2000US-0217487.
2000US-0218290.
2000US-0218290.
2000US-022963.
2000US-0224518.
2000US-0225213.
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2000US-0229287.
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2000US-0227009.
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2000US-0225267.
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02-OCT-2000;
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14-AUG-2000;
18-AUG-2000;
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07-JUL-2000;
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22-AUG-2000;
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17-MAR-2000;
18-APR-2000;
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Claim 11; SEQ ID No 312; 577pp; English.

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Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                              20000S-0244617.
20000S-0246474.
20000S-0246477.
20000S-0246477.
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20000S-0246524.
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2000US-0249244.
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2000US-0249264.
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2000US-0241808.
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2000US-0241826.
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2000US-0250160.
2000US-0250391.
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2000US-0251988.
2000US-0256719.
2000US-0251479.
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N-PSDB; AAS31233.
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17 - NOV - 2000;
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (5Ps). The novel human secreted extracellular matrix proteins (5Ps). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to dreat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used to down regulate expression and activity of antagonists may also be used to down regulate expression and activity of antagonists may also be used to down regulate expression and activity of antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis, cancers and hyperproliferative disorders (e.g. fur melanomas, neoplasms of the breast or liver, Sezary syndrome and caucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
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49.0%; Score 938.5; DB 22; Length
Best Local Similarity 52.1%; Pred. No. 3.8e-91;
Matches 185; Conservative 59; Mismatches 104; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 collular proliferation, modulate polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cell adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, plumonary conquesting interaction of cells as than and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as includent to the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW 59
                                                                                                                                                                                                                                                                                                                                                                                             Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.0%; Score 937.5; DB 21; Length 487; 50.1%; Pred. No. 3.7e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115;
                                                                                                                                                                                                                                                                                                  Fraser CC;
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                                                                                                                                                                                                                                                                                                  Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                             01-MAR-2000; 2000WO-US05226.
                                                                                                                                                                                                                        99US-0122458.
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                                                                                                                                                                                                                                                                                                  Holtzman DA,
                                                                                                                                                                                                                                                                                                                                         2000-579269/54.
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Best Local Similarity
Matches 186; Conserv
                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA75160
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                                                                                                                                                                                                                      01-MAR-1999;
                                                                                                                                          08-SEP-2000
                                                                                                                                                                                                                                                                                                    Barnes TM,
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; ocllular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; ocdema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; isohemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; hazhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                  NDGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPA 359
238 vltgravtsishdgsvlctftanstytksekpvsigpssilcpapvlnkdgetlevsisy 297
                                                                           Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a murine TANGO 216 polypeptide.
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/note= "transnmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "extracellular domain"
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ote= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       AAB18448 standard; Protein; 487 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2001 (first entry)
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98.
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34..487
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318..34
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N-PSDB; AAA75150.
                                                                                                                                                         360 --- EESEENKI 367
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proliferation also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 261, TANGO 262, and TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular adhesion. The proteins can be used to treat any von Millebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation modulate disorders, such as cancer, modulate the proliferation, differentiation, and promoter cellular interactions, modulate the proliferation, differentiation, from marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchists, bronchial asthma and bronchisctasis, intestinal disorders, spleen associated diseases, modulate the disorders spleen associated diseases, modulate the cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders such as ischemic heart disease, cardiovascular disorders be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's brain cancers, hydrocephalus, and viral meningitis, and treat hepatic
                              The present sequence represents a murine TANGO 216 polypeptide. The
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                                                                                                           300 NDGLSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPA 359
                                                                                                                                                                                                                                                                                                    MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG 179
                          Gaps
                                                             1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW 59
                                                                                                                                                                                                        180 VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV
                                                                                                                                                                                                                                         240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM
                         7;
48.9%; Score 936.5; DB 21; Length 487; 50.1%; Pred. No. 4.7e-91; ive 63; Mismatches 115; Indels 7;
           4.7e-91;
ches 115; Indels
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            Similarity
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  Query Match
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TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion;

A murine TANGO 216 polypeptide clone.

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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 cellular differentiation and/or modulate cellular adhesion. The polypeptides can be used to endulate cellular adhesion. The proteins can be used to treat any von Wilebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, modulate cell adhesion in proliferation, and/or function of cells modulate the proliferation, differentiation, and/or function of cells and hematopoietic associated diseases and disorders, atelectasis, and hematopoietic associated diseases and disorders, apleen associated diseases, modulate renal disorders, treat concittis, bronchial asthma and bronchiactasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral codema, hydrocephalus, brain hermiations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, inflammations, hydrocephalus and encephalitis, and treat hepatic disorders, it was concert, the present sequence does not appear in the specification; it was
                    hematopoletic associated disease, atelectasis; pulmonary congestion; ocedems; emphysema; chronic bronchitis; bronchial asthma; bronchies intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxplasmosis; parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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cell trafficking; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser CC;
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    Willebrand factor-associated disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
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N-PSDB; AAA75162.
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Best Local Similarity
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                                                                                                                                                                                                               240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                                                                                                                                              NDGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A murine TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                   AAB18459 standard; Protein; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-579269/54.
                                                                                                                                                                                                                                                                                                            358 apmeeeeedpl 368
                                                                                                                                                                                                                                                                          ---EESEENKI 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA75161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200052022-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1999;
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that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as isobmanic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bydrocephalus, brain herniations, istrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.8%; Score 933.5; DB 21; Length
49.9%; Pred. No. 9.9e-91;
Live 64; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB01428 standard; Protein; 381 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 49.9
Matches 185; Conservative
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WO200039284-A1.

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                                                                                                                                                                                                                                                         Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 909; DB 21; Length 381;
Pred. No. 2.8e-88;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 27; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.5%;
                                                                                                                                    (MILL-) MILLENNIUM PHARM INC
                                                                                              98US-0223546.
                                                                 99WO-US31025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.3
Matches 175; Conservative
                                                                                                                                                                                                        WPI; 2000-465743/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AA;
                                                                                                                                                                                                                          N-PSDB; AAA47479
                                                                                                  30-DEC-1998;
                                                               23-DEC-1999;
                                                                                                                                                                     Holtzman DA;
                              06-JUL-2000
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Search completed: August 9, 2002, 10:32:10 Job time: 129 sec

247 RHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFI 306

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ô g ö 307 SSSVIITTHCSDGSILAIALLILFLLLALAWWFWPLCCTVIIKEVPPPAEESEE 364

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 9, 2002, 10:33:17 ; Search time 31.3 Seconds (without alignments) 455.233 Million cell updates/sec Run on:

US-09-970-076-2 1914 1 MATAERRALGIGFQWLSLAT......VIIKEVPPPPAEESEENKIK 368 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	x2 h	mus m	рошо	homo	homo) homo	P13944 gallus gall	mus	mus	mus m		gallu	caenc		Q91145 notophthalm	gallu	homo sa		homod	mus m	Q02788 mus musculu	mus	mns		gallu	homo	homo	32 homo	drosoph	35	16893 plasm	12110 homo	P12111 homo sapien
SUMMARIES	ΩI	ATR_HUMAN	ATR_MOUSE	CMG2_HUMAN	ITAD_HUMAN	ITAM_HUMAN	ITAX_HUMAN	CA1C_CHICK	ITAM_MOUSE	CA1C_MOUSE	CO2_MOUSE	CA1C_HUMAN	CA1E_CHICK	YNX3_CAEEL	CAMA_HUMAN	CA1C_NOTVI	MTN3_CHICK	CFAB_HUMAN	MTN9_HUMAN	CA17_HUMAN	CFAB_MOUSE	CA26_MOUSE	CAMA_MOUSE	MTN4_MOUSE	MTN2_MOUSE	CAMA_CHICK	ITAH_HUMAN	MTN4_HUMAN	MTN3_HUMAN	ROP_DROME		TRAP_PLAFA	CA26_HUMAN	CA36_HUMAN
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Q9KOn4 neisseria m Q90615 gallus gall P65199 homo sapien P15989 gallus gall Q28902 oryctolagus P38570 homo sapien P18614 rattus norv Q60677 mus musculu P58079 caulobacter O43405 homo sapien Q91yq9 neisseria m	
DNAK_NEIMB ITA1_CHICK ITA1_HUMAN CA36_CHICK CA1C_RABIT ITA4_HUMAN ITA4_RAT ITAA_RAT ITAA_ROUSE HUTI_CAUCR COCH_HUMAN DNAK_NEIMA	
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642 285 1151 3137 639 1179 1180 1167 401 550 642	
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97.5 97.5 97.9 97.9 95.5 92.5 92.5	
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ALIGNMENTS

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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).

NEDDD -> NRIK (IN ISOPORM 2).

MISSING (IN ISOPORM 2).

NEKPPESUDTYLLCPAPILKEVGMKAALQV -> SKSLQSP

MISSING (IN ISOPORM 3).

MISSING (IN ISOPORM 3).

DGSILABILLELL -> LHKIASGPTTAACME (IN
                                                                                                                                                                                                                                                                                                                                                               241 VRGNGFRHARNYDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                                                                                                                                                                                                                                                  61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                                                                                                                                                          61 BIYYEVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                             Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                             181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                    241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                        Length 564;
                                                                                                                                             ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
                                                                                                                                                                                                                                                                                       Indels
                                                                                                          ANTRAX TOXIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                          MISSING (IN ISOFORM 4).
B118A00AD5DF2233 CRC64;
                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
VWFA.
                                                                                                                                                                                                                                                                        Score 1894; DB 1; I
Pred. No. 3.1e-147;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 AA.
  modified and this statement is not removed. entities requires a license agreement (See h
                                                                                                                                                                                                                                    ISOFORM 4).
                                                                     InterPro: IPR002035; vWFA.
SMART; SM00327; vWA; 1.
PROSITE; PS50234; vWFA; 1.
Receptor; Transmembrane; Glycoprotein;
                 or send an email to license@isb-sib.ch)
                                                                                                   POTENTIAL
                                       EMBL; AK025429; BAB15128.1; ALT_INIT.
EMBL; AK001463; BAA91707.1; ALT_FRAME.
EMBL; BC012074; AAH12074.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                         99.0%; Sco
100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                   MM;
                                 EMBL; AF279145; AAK52094.1; -.
                                                                                                                                                                                                                                                   62789
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 364; Conservative
                                                                                                                                  2564
368
368
166
1184
1262
262
262
297
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ESEE 364
                                                                MIM; 606410;
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TRANSMEM
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CARBOHYD
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ID ATR_MO
AC Q9CZ55
DT 01-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA MEDLINE-21U85001; PUDMED=1121/851;

RA KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Pukunishi Y., Konoo H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Salto T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

RA Gadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Dolffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Moshima J., Mazzarelli J., Mombaerts P.,

RA Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibbar Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RA Hayashizaki Y.;

RA Hayashizaki Y.;

Ra Hayashizaki Y.;

Ruture 409:685-690(2001).

CC -!- SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis (By similarity).

CC -!- SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis (By similarity).

CC -!- SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis (By similarity).

CC -!- ALTERNATUR PRODUCTS: 2 isoforms; 1 (shown here) and 2; seem to CC -!- DOMARIN: Binding to PA seems to be effected through the VWA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                    Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinzler K.W., St Croix B.; "Cell surface tumor endothelial markers are conserved in mice and
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Antrax toxin receptor precursor (Tumor endothelial marker 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDIINE-2143268; PubMed-11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinaler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTRAX TOXIN RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
SIMILARITY: BELONGS TO THE ATR FAMILY.
SIMILARITY: CONTAINS I VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . EQUENCE OF 88-562 FROM N.A. (ISOFORM 2).
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer Res. 61:6649-6655(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF378762; AAL11999.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK013005; BAB28591.1
MGD; MGI:1919432; Atr.
InterPro; IPR002035; VWFA.
PROSTIE; PS50234; VWFA; II.
Receptor; Transmembrane; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562
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SIGNAL
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TRANSMEM
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Noti J.D., Johnson A.K., Dillon J.D.;
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215
236
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213
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34
216
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211
386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 KEEEEE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 AEESEE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITAD_HUMAN
                                                                   DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
SEQUENCE
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ITAD_HUMAN
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GRCINFTRYNNSQPAKYPLNYTYPPSSPPAPIYTPPPAPAPHCPPPAPSAPTPPIPSPFSTLPPPPPQAPPRNRAPPPSRPPPROPPSSFLERAFQ (IN ISOFORM 2).
GAC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21539596; PubMed-11683410; Bell S. E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Ball S. E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.A., Davis G. E.;

"Differential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.";

J. Cell Sci. 114:2755-2773(2001).

SUBCELLULAR LOCATION: Type I membrane protein (Probable).

SUBCELLULAR LOCATION: Type I membrane protein (Probable).

SIMILARITY: BELONGS TO THE ATR FAMILY.
                                                                                                                                                                                                                 248
                                                                                                                                                                                                       LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                                                                                                                                                   EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
                                                                                                                                                                                                                                                                                                                                            ARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS 308
                                                                                                                                                                       Gaps
                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
                                                                                                                                                           LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ
                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                 Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capillary morphogenesis protein-2 precursor (CMG-2).
                                                                                                               Score 1793; DB 1;
Pred. No. 5.6e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 AA
                                                                                                                                      Mismatches
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Σ
                                                                                                               93.7%;
96.1%;
                                                                              62308
                                                                                                                                      Conservative
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                                                                                                                          Similarity
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SEQUENCE FROM N.A.
 164
182
260
477
                                                                              562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMG2_HUMAN
P58335;
                                                                                                               Query Match
Best Local Simi
Matches 342;
CARBOHYD
CARBOHYD
CARBOHYD
                                                                              SEQUENCE
                                   VARSPLIC
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GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 XYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG 302
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uunton D.E., Gallatin W.M.;
novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPP----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D) (CD11d) (ADB2)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       (POTENTIAL).
                                                                                               CAPILLARY MORPHOGENESIS PROTEIN-2
                                                                                                                                                                                                                                                                                                                                                                     69; Indels 110;
                                                                                                                                                                                                                                                                                                                    Length 386;
                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                       ·LINKED (GLCNAC. . .) (P
0F9B2D6688EAB17A CRC64;
                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.0%; Score 651; DB 1; 38.8%; Pred. No. 7.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin alpha-D precursor (Leukointegrin alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   013349; Q15575; Q15576;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1162 AA
                                                                                                                                                                                                                                                                                                                                                                     45; Mismatches
                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                       N-LINKED
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MEDLINE-20187620; Pubmed-10722744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE~Spleen;
MEDLINE~96111956; PubMed-8777714;
EMBL; AY040326; AAK77222.1; -. PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                 MW.
                                         Transmembrane; Glycoprotein; SIGNAL 1 33
                                                                                                                                                                                                                                              42918
                                                                                                                                                                                                                                                                                                                      Query Match 34.0°
Best Local Similarity 38.8°
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL.

-!- INES AND SUBSETS OF PERIPHERRAL BLOOD LEUKOCYTES AND STRONGLY ON TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN TISSUE-SPECIALIZED CELLS, INCLUDING NACROPHAGES FOAM CELLS WITHIN THEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.

-!- DOMAIN: THE INTEGRIN !- DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH !- DOMAINS TO THE INTEGRIN ALPHA CHAIN FAMILY.

-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                   SECURICE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE-96257236; PubMed-866289; Mong D.A., Davis E.M., LeBeau M., Springer T.A.; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human beta 2-integrin alpha subunit.";
                                                                                                                                                                                                                                                               MEDLINE-99059842; PubMed-9841932; Graphinsky S.A., Michael Gallatin W., Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.; "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-1).";
"Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Spl and Sp3."; J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIANDE MAIN TOTAL NOTE:

MEDIANDE-99370002; PubMed=10438935;

MEDIANDE-99370002; PubMed=10438935;

Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;

Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;

"The leukocyte integrin alpha D berd 2 binds VcAM-1: evidence for a phinding interface between I domain and VcAM-1.";

J. Immunol. 163:1984-1990(1999).

-I-FUNCTION: INTEGRIN ALPHA-D/BETA-2 IS A RECEPTOR FOR ICAM3 AND VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS USANING LIPOPROTEINS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOODERON MINE PLAYORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01839; FG-GAP; 5.
Pfam; PF000357; integrin_A; 1.
Pfam; PF000957; wwa: 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; WWRDDOMAIN.
SMART; SM00191; INT_Alpha; 4.
SMART; SW001327; WWA: 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIN; 602453; ...
Interpro; IPR000413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U37028; AAB38547.1; --
EMBL; U40275; AAB60654.1; --
EMBL; U40275; AAB60635.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40279; AAB60638.1; --
EMBL; U40278; AAB60638.1; JOINED.
EMBL; AF1878
                                                                                                                                                                                                                                                                                                                                                                                                                     Exp. Med. 188:2187-2191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH VCAM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
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232 LTVVTQLFHHKNGARKSAKKILIVITDGQKYKDPLEYSD-VIPQAEKAGIIRYAIGVGHA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 NETQLAR-----IADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 FQGPTARQELNTISSAPPQDHVFKV-DNFAALGSIQKQLQEK----IYAVEGTQSRASSS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 ERASEQIYYENRQGYRTA-SVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLP----GGDTYMHEGF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 FQVVVRGNGFRHARNVDRVLC----SFKINDS------VTLNEKPFSVEDTYL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 IGFQWLSLATLVLICACQGGRREDGGPAC-YGGFDLYFILDKSGSV-LHHWNEIYYFVEQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%; Score 159.5; DB 1; Length 1162; 23.4%; Pred. No. 4.4e-05; Live 54; Mismatches 124; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Signal; Repeat; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F296A1A35455D77D CRC64;
                                                                                                 INTEGRIN ALPHA-D.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                          CYTOPLASMIC (POTENTIAL). FG-GAP 1. FG-GAP 2. VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN REF. 2).
GHPW -> ATP (IN REF. 2)
                                                                                                                                                                                                            FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
FG-GAP
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    SEQUENCE FROM N.A.
MEDLINE-88190151; PubMed=2833753;
Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
Annout M.A., Remold o'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
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leukocyte adhesion glycoprotein Mol: chromosomal localization and
homology to the alpha subunits of integrins.";
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MEDLINE-93123748; PubMed-8419480;
Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
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Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
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01-UUL-1989 (Rel. 11, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1906 (Rel. 34). Last sequence update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subbunit) (CR-3 alpha chain) (CDl1b) (Leukocyte adhesion receptor MO1)
ITGAM OR CR3A OR CD11B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "CDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits."; Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shelley C.S., Arnaout M.A.; "The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
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Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991)
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MEDLINE-87076671; PubMed=3539202;
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GRANULOCYTES.

-!-DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

-!-SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

-!-SIMILARITY: CONTAINS I VWFA DOMAIN.

-!-SIMILARITY: CONTAINS 7 FG-GAP REPEATS.

-!-DATABASE: NAME-PROW; NOTE-CD quide CD11b entry;

WWM-"http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
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Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).

-!- FONCTION: INTEGRIN ALPHA M/BETA-2 IS IMPLICATED IN VARIOUS
ADHESIVE INTERACTIONS OF MONOCYTES, MACROPHAGES AND GRANULOCYTES
AS WELL AS IN MEDIATING THE UPTAKE OF COMPLEMENT-COATED PARTICLES.
IT IS IDENTICAL WITH CR-3, THE RECEPTOR FOR THE IC3B FRAGMENT OF
THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECOGNIZES THE R-G-D
PEPTIDE IN C3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR
FIBRINGEN, FACTOR X AND ICAM. IT RECOGNIZES PI AND P2 PEPTIDES
OF FIBRINGEN CAMPA CHAIN.
                                                                 Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin
                                                                                                                                                                                                                                                                                                                   Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.; "Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Experimental support for a beta-propeller domain in integrin alpha-
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MEDLINE-98362595; PubMed-9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Marines R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Catton binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-M ASSOCIATES WITH BETA-2. SUBCELLULAR LOCATION: TYPE I membrane protein. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
MEDLINE=95171458; PubMed=7867070;
                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334 MEDLINE=96363671; PubMed=8747460;
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MEDLINE=98226734; Pubmed=9560195;
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Cell 80:631-638(1995).
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[2]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              p150,95 molecule.
                                                                                                                                                                            NCBI_TaxID=9606;
                      ITAX_HUMAN
P20702:
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 FTFKEFQNNPNPRSLVKPIIQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED---- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS5024; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; 3D-structure; Repeat; Magnesium; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 145.5; DB 1; Length 1152;
26.2%; Pred. No. 0.0006;
.ive 45; Mismatches 81; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). FG-GAP 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
InterPro; IPR02035; vWFA.
Pfam; PF01839; FG-GAP; 5.
Pfam; PF00095; vwa; 1.
PRIMTS; PR01185; INTEGRINA.
PRIMTS; PR001185; INTEGRINA.
PRIMT; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
                               L. S52114, AAB24821.1; JOINED.
L. S52180, AAB24821.1; JOINED.
L. S52181, AAB24821.1; JOINED.
L. S52181, AAB24821.1; JOINED.
L. S52181, AAB24821.1; JOINED.
L. S52191, AAB24821.1; JOINED.
L. S522191, AAB24821.1; JOINED.
L. S52213, AAB24821.1; JOINED.
L. S52213, AAB24821.1; JOINED.
L. S52215, AAB24821.1; JOINED.
L. S52216, AAB24821.1; JOINED.
L. S52216, AAB24821.1; JOINED.
L. S52221, AAB24821.1; JOINED.
L. S52221, AAB24821.1; JOINED.
L. S52221, AAB24821.1; JOINED.
L. S52221, AAB24821.1; JOINED.
L. S52222, AAB24821.1; JOINED.
L. S52224, AAB24821.1; JOINED.
L. S52224, AAB24821.1; JOINED.
L. S52226, AAB34821.1; JOINED.
L. S52221, AAB34821.1; JOINED.
L. S52221, AAB34821.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                     CarbBank; CCSD:33581; -. CarbBank; CCSD:33582; -. CarbBank; CCSD:33584; -.
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1152
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Signal; 3D-structure;
SIGNAL
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1BHO; 18-NOV-98.
1BHQ; 18-NOV-98.
1IDN; 25-NOV-98.
1IDN; 25-NOV-98.
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TRANSMEM
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 100
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SMART; SM00191; Int_alpha; 4.
SMART; SM00191; Int_alpha; 4.
SMART; SM00242; VWA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
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-> D (IN REF. 2).
6C4E19CC3F62A473 CRC64;
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EXTRACELLULAR (POTENTIAL)
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BY SIMILARITY.

CECNAC.

CONTROL GLCNAC.

CONTROL 
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                                                      InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                              Signal; Magnesium; Calcium; Repeat.
EMBL; M29486; AAA51620.1; JOINED
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                                                                                                                                                           Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                  CarbBank; CCSD:33581; -. CarbBank; CCSD:33582; -. CarbBank; CCSD:33584; -.
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1128
1163
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                PIR; A36584; RWHUIC.
HSSP; P11215; 1A8X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query ...
Best Local Similar
                                                                                                       MIM; 151510;
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TRANSMEM
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-WHITE LEGHORN:
MEDLINE-92011862; PubMed-1918137;
Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,
Nishida Y., Obara M., Kimata K.;
"The complete primary structure of type XII collagen shows a chimeric
molecule with relterated fibronectin type III motifs, von Willebrand
factor A motifs, a domain homologous to a noncollagenous region of
type IX collagen, and short collagenous domains with an Arg-Gly-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE SPLICING.
MEDLINE-93370322; Pubmed-7642694;
MEDLINE-93370322; Pubmed-7642694;
Roch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Roch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Earge and small splice variants of collagen XII: differential
expression and ligand binding.";
J. Cell Biol. 130:1005-1014(1995).
-!- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
LOCALIZED IN THE PERIFIBRILLAR MATRIX.
-!- SUBJUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 KDa OF
NONTRIPLE-HELICAL SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-1283 FROM N.A. (SHORT FORM), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen "Type XII collagen. A large multidomain molecule with partial homology to type IX collagen."; Use 1564:19772-19778(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 2960-3076 FROM N.A.
MEDLINE-87317590; Pubmed-3476925;
Gordon M.K., Gerecke D.R., Olsen B.R.;
"Type XII collagen: distinct extracellular matrix component discovered by cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
MEDIINE=293042014; PubMed=1420368;
Trueb J., Trueb B.; Trueb B.;
The two splice variants of collagen XII share a common 5'
Biochim. Biophys. Acta 1171:97-98(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794
                                                                                                                                                                                                                                                                                                                                  P13944; 004509; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 35, Last sequence update) 01-NOY-1997 (Rel. 41, Last annotation update) collagen alpha I(XII) chain precursor (Fibrochimerin).
                                                 | ||: | : : : | | | | : : || | | 319 FDALKDIQNQLKEK----IFAIEGTETTSSSSFELEMAQEGF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
205 FQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90062079; PubMed-2584192;
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                                                                                                                                                                                                                                                                                                       STANDARD;
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 17, Last sequence update)
01-MFAR-2002 (Rel. 41, Last annotation update)
11-MEGrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLYFILDKSGSV-LHHWNEIYYEVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTHELICAL REGION (NC2).

TRIPLE-HELICAL REGION (NC1).

WITH 2 IMPERETIONS.

NOTHELICAL REGION (NC1).

ASP/GLU-RICH (ACIDIC).

ASP/GLU-RICH (BASIO).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

M-LINKED (GLCNAC. .) (POTENTIAL).

MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 143; DB 1; Length 3124; Pred. No. 0.0035;
NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              094285AFE7F346CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                F -> S (IN REF. 4).

-> E (IN REF. 4).

-> A (IN REF. 2).

L -> F (IN REF. 2).

V -> F (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Scoll 26.1%; Pred. No. vol. 51; Mismatches
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11188
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2803
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Best Local Similarity
Matches 65; Conserva'
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                                                                                                                                                                                                                                                                                                                                                                                                DR EMBL; X61024; CAA43788.1; --
DR EMBL; X61024; CAA43788.1; --
DR EMBL; X61024; CAA43788.1; --
DR EMBL; M17375; AAA48718.1; --
DR EMBL; X67327; CAA47744.1; --
DR EMBL; X67327; CAA47744.1; --
DR PIR; A24037; A24085.
DR PIR; A34485; A34485.
DR PIR; A34485; A34485.
DR PIR; A2403961; FN_III.
DR INCEPPO: IPR000361; FN_III.
DR INCEPPO: IPR003962; FNII_repeat.
DR INCEPPO: IPR003962; FNII_repeat.
DR INCEPPO: IPR003129; VWFA.
DR INCEPPO: IPR003129; VWFA.
DR Pfam; PF00131; COllagen; 4.
DR Pfam; PF00041; Fn19; 1.
DR Pfam; PF00041; Fn19; 1.
DR Pfam; PR00041; FN19EIII.
DR PRINTS; PR00041; FN19EIII.
DR PRINTS; PR00014; FN19EIII.
DR PRINTS; PR00016; FN3; 1.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00210; TSPN; 1.
DR PROSITE; PS50334; VWFA.
DR SMART; SM00210; TSPN; 1.
DR PROSITE; PS50334; VWFA.
DR PROSITE; PS5034; VWFA.
DR PROSIT
     C -1- TISSUE SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS,
LIGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE
TISSUES CONTAINING TYPE I COLLAGEN.
C -1- DOMAIN: THIS SEQUENCE DEFINES FLUE DISTINCT DOMAINS, TWO TRIPLE-
HELICAL DOMAINS (COLLAND COL2) AND THREE NONTRIPLE-HELICAL
DOMAINS (NIL, NC2, AND NC3).
C -1- PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
EACH END.
C -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
C -1- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
C -1- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
C -1- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
C -1- SIMILARITY: CONTAINS 18 FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACITY) FAMILS.
C -1- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
C -1- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
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FIBRONECTIN TYPE-III 4
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Signal; Calcium;
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Q60847;
      Integrin;
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"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1
"It is law. 14.140-14.2(1985).
"It is learned and unexpected relation to leukocyte interferon.";
ADHESIVE INTERATING THE UPTAKE OF COMPLEMENT-COATED PARTICLES.
THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECGNIZES THE R-G-D
PEPPIDE IN C3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR
THE THIRD COMPLEMENT COMPONENT. IT RECOGNIZES P1 AND P2 PEPTIDES
OF FIBRINGEN, FACTOR X AND ICAMI. IT RECOGNIZES P1 AND P2 PEPTIDES
OF FIBRINGEN, PACTOR X AND ICAMI. IT RECOGNIZES P1 AND P2 PEPTIDES
OF FIBRINGEN GAMMA CHAIN. ALPHA-M/BETA-2 PLAY A CRITICAL ROLE IN
MAST CELL DEVELOPHENT AND IN IMMONE COMPLEX-MEDIATED
CLOMERULONEPHISTIS. MICE EXPRESSING A NULL MUTATION OF THE ALPHA-M
SUBUNIT GENE DEMONSTRATE INCREASE IN NEUTROPHIL ACCUMULATION, IN
RESPONSE TO A IMPALRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT
OPPER THE THOUSE OF THE THOUSE THE THAT THESE MICE DEVELOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mac-1 alpha chain reveals homology ditional domain related to von
                                                                                                                                                                                         SEQUENCE OF 11-45 FROM N.A.
STRAIN=BALB/C; TISSUB-Spleen;
MEDLINE-86287312; PubMed-294240;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UBESITY.
-! SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M ASSOCIATES WITH BETA-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                     "Amino acid sequence of the murine Mac-1 al
with the integrin family and an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD: MGI:96607; Itgam.
Interpro: IPR000413; Integrin_alpha.
Interpro: IPR002035; vWFA.
Pfam: PF01839; FG-GAP; 5.
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PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE OF 17-28.
MEDLINE-85188276; PubMed-3887182;
[1]
SEQUENCE FROM N.A.
MEDLINE-88312584; PubMed-3044779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PR01189; INTEGRINA.
PRINTS: PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00357; integrin_A; 1. Pfam; PF00092; vwa; 1.
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                                                                                                                                                   EMBO J. 7:1371-1378(1988).
                                                                                                                                 Willebrand factor.
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    DARARAR RARAR ``

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355
 150 DIVFLIDGSGSI----NNIDF---QKMKEFVSTVMEQFKKSKTLFS-----LMQYSDEFR 197
 ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 149
 :: | | | | | ::::| | 138 IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT 257
 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP 200
 201 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
 Gaps
 44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 98
 315 V-DNFEALNTIQNQLQEK----IFALEGTQTGSTSSFEHEMSQEGF------
 (POTENTIAL). (POTENTIAL). (POTENTIAL).
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 (POTENTIAL)
(POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 16;
Cell adhesion; Receptor; Glycoprotein; Transmembrane;
 (POTENTIAL
 261 INDSVTLNEKPFSVEDTYLLCPAPILKEVG----MKAALQVSMNDGLSFISSS 309
 Query Match 7.4%; Score 141; DB 1; Length 1153; Best Local Similarity 24.2%; Pred. No. 0.0014; Matches 71; Conservative 50; Mismatches 96; Indels 76
 178DB988AECB0343 CRC64;
 INTEGRIN ALPHA-M.
EXTRACELLULAR (POTENTIAL)
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 CYTOPLASMIC (POTENTIAL).
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 PRT; 3067 AA
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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Lev. Dyn. 204:432-445(1995).

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Lev. Dyn. 204:432-445(1995).

CONTAINING FIBRILS, THE COLL DGNAIN COULD BE ASSOCIATED WITH THE CONTAINING TIBRILS, AND THE COLZ AND NG3 DOMAINS MAY BE COLALIZED IN THE PERRIFIBALLER MATRIX (BY SIMILARITY).

LOCALIZED IN THE PERRIFIBALLER MATRIX (BY SIMILARITY).

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LOCALIZED IN THE PERRIFIBALIZE BY SIMILARITY).

LOCALIZED IN THE PRODUCED BY ALTERNATIVE SPLICING. THE FIRAL TISSUE SOME THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTECCHIVCAN.

LISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTECCHIVCAN.

SKIN, CORNEA, SCLERA, BLOOD VESSELS, AND PERIOSTEUM.

CHEDOMENTAL STAGE: LONG FORM OF COLLAGEN XII, XIIA, IS THE STAGES (EDT AND THE SHORT FORM, XIIB, BECOMES THE MAJOR PRODUCT, THE LONG SPLICE FORM. AS THE SHORT FORM BECOMES THE MAJOR PRODUCT, THE LONG SPLICE FORM.

CHARLES THE SHORT FORM BECOMES THE MAJOR PRODUCT, THE LONG SPLICE FORM.
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 PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN-SWISS WEBSTER, AND C57BL/6J; TISSUE-Skin;
BEDLINE-96107061. PubMed-8601036;
Boehme K., ii Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic development.";
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 -!- PTM: GLYCÓŚYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (PACIT) PAMILY.
-!- SIMILARITY: COWTAINS 4 WWFA DOMAINS.
-!- SIMILARITY: CONTAINS 10 FIBRONECTIN TYPE III-LIKE DOMAINS.
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain precursor.
 MGD: MGT:88448; Coll2al.
MGD: MGT:88448; Coll2al.
Interpro: IPR003067; Collagen.
Interpro: IPR003961; FN_III.
Interpro: IPR003129; FN_III.
Interpro: IPR003129; TSPN.
Interpro: IPR002035; VWFA.
Ffam; PF001391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; Vwa; 4.
Pfam; PR0045; VWEADOMAIN.
SMART; SM00060; FN3; 16.
SMART; SM0010; TSPN; 1.
 EMBL; U25652; AAA99719.1; -.
HSSP; P02751; 1TTF.
 Mus musculus (Mouse)
 NCBI_TaxID=10090;
 SIMILARITY)
 BIRTH
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12;
 44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
 QIRQGLEELQKVL----PGGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 153
 Gaps
PROSITE; PS50234; VWFA; 4. Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
 WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NC1).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
 . .) (POTENTIAL)
 (POTENTIAL)
 26;
 (POTENTIAL)
 7.3%; Score 139; DB 1; Length 3067; 30.3%; Pred. No. 0.0072; ive 37; Mismatches 75; Indels 28
 SIMILARITY).
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 HYDROXYLATION (BY SIMILARITY).
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 NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
 TRIPLE-HELICAL REGION (COL2) WITH 1 IMPERFECTION.
 COLLAGEN ALPHA 1(XII) CHAIN.
 I SOFORM)
 FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-III 11.
FIBRONECTIN TYPE-III 11.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
 (GLCNAC. . .)
 (GLCNAC. . .)
 NONHELICAL REGION (NC3)
 FIBRONECTIN TYPE-III 1.
 FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 7
FIBRONECTIN TYPE-III 7
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 Ouery Match 7.3%; Score 139; DB Best Local Similarity 30.3%; Pred. No. 0.007
Matches 60; Conservative 37; Mismatches
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N-LINKED (
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 VWFA 2
 AA; 334094
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M60578;
M57891;
 M60569;
 M60574;
 M60605;
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 MEDLINE-91035430; PubMed-2229060; MEDLINE-91035430; PubMed-2229060; MEDLINE-91035430; PubMed-2229060; MEDLINE-91035430; MEDLINE-91035430; Metsel R.A., Colten H.R.; Murine complement C2 and factor B genomic and cDNA cloning reveals of ferent mechanisms for multiple transcripts of C2 and B."; J. Biol. Chem. 265:19040-19046(1990).

J. Biol. Chem. 265:19040-19046(1990).

THE COMPLEMENT SYSTEM IS CLEAVED BY ACTIVATED FACTOR C1 INTO TWO FRAGMENTS: C2B AND C2A. C2A. C2A. A SENINE PROTEASE, THEN COMPLENDENT FACTOR 4B TO GENERATE THE C3 OR C5 CONVERTASE.

COMPLEMENT FACTOR 4B TO GENERATE THE C3 OR C5 CONVERTASE.

CATALYTIC ACTIVITY: CLEAVES C3 IN THE ALPHA-CHAIN TO YIELD C3A AND C5B. BOTH CLEAVES C5 IN THE ALPHA-CHAIN TO VIELD C3A AND C5B. BOTH CLEAVES C5 IN THE ALPHA-CHAIN TO VIELD C3A AND C5B. BOTH CLEAVES C5 IN THE ALPHA-CHAIN TO VIELD C5A AND C5B. BOTH CLEAVES C5 IN THE C-TERMINAL OF AN ARGININE RESIDUE.
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 SSDAF---RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVED-FDAFQRI
 PROTEIN.
-!- SIMILARITY: WITH COMPLEMENT FACTOR B.
-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) DOMAINS.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
 AAA37380.1; JOINED.
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 212 IHSILKKSCIEI---LAA 226
 613 SFVLTQSICLRIEQELAA 630
 AAA37380.1;
AAA37380.1;
AAA37380.1;
 EMBL; M60579; AAA37380.1;
 AAA37380.1;
 AAA37380.1;
 AAA37380.1;
 AAA37380.1;
 AAA37380.1
 AAA37380.1
 STANDARD;
 AAA37380.1
 Mus musculus (Mouse)
 NCBI_TaxID=10090;
 EMBL; M60565; R
EMBL; M60566; R
EMBL; M60567; R
EMBL; M60568; R
 M60577;
M60578;
 M60570;
M60571;
 EMBL; M60564;
 M60572;
 M60573;
 M60574;
 M60576;
 CO2_MOUSE
P21180;
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16;
 Complement pathway; Plasma; Glycoprotein; Hydrolase; Serine protease;
Signal; Repeat; Sushi; Alternative splicing.
SIGNAL 18
 Gaps
 CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

BY SIMILARITY.

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N-LINKED (GLCNAC...) (POTENTIAL).

 RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
 74;
 6.8%; Score 131; DB 1; Length 760;
23.2%; Pred. No. 0.0054;
iive 56; Mismatches 115; Indels
 (IN SHORT ISOFORM)
 D7DE9DEF4DBA48D9 CRC64
 COMPLEMENT C2B FRAGMENT COMPLEMENT C2A FRAGMENT
 SERINE PROTEASE.
CHARGE RELAY SYST
CHARGE RELAY SYST
 COMPLEMENT
 SUSHI 1.
SUSHI 2.
SUSHI 3.
 MISSING
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000436; Sushi_SCR_CCP
InterPro; IPR001254; Trypsin.
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 PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS00134; TRYPSIN_LHIS; 1. PROSITE; PS00135; TRYPSIN_SER; 1. PROSITE; PS50234; VWFA; 1.
 Pfam; PF00089; trypsin; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PF00092; vva; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00020; Tryp_SPC; 1.
 MW.
AAA37381.1;
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AAA37381.1;
 AAA37381.1;
AAA37381.1;
AAA63294.1;
 84726
 AAA37381.1;
AAA37381.1;
 InterPro; IPR002035; vWFA
 Query Match 6.8
Best Local Similarity 23.2
Matches 74; Conservative
 250
250
760
90
150
211
2211
760
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570
689
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89
136
149
197
27
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117
32
340
 49
94
122
156
182
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37
111
117
478
478
663
 HSSP; P00757; ISGF.
MEROPS; S01.194; -.
MGD; MGI:88226; C2.
 PIR; A38876; C2MS
 19
19
251
21
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155
1155
1155
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270
689
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RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

REA GETECKE D.R., Olson P.F., Olson B.R., Burgeson R.E.;

GETECKE D.R., Olson P.F., Olson B.R., Burgeson R.E.;

And assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX)

RT conclagen (COL9A1), and alpha 1(XIX) collagen (COL12A1), alpha 1(IX)

RT collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human (COLTAGEN INTERACTS WITH TYPE I COLLAGEN INTERACTS WITH TYPE I COLLAGEN

RL contransing FIREILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE COLTAGEN INTERACTS WITH TYPE I COLLAGEN

CONTAINING FIBEILS, AND THE COLL AND NC3 DOMAINS MAY BE SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF INCALLAGEN IN THE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT PORD COLLAGED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGED XITHE LONG VARLANT IS A PROTEOGLYCAN.

C. - ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT COLLAGEN XII MAY CONTAINING TISSUES: BOTH SHORT CALLAGEN IN AMION, CHORINA, SKELETAL SHORT AND LONG ISOFORM OR ANY COMBINATION OF LONG AND SHORT COLLAGEN SAPEL FICTURE, AND INTERSITY HE LONG VARLANT IS A PROTEOGLYCAN.

C. ISOFORM IS FOUND IN UNG, PLACENTA, KIDNEY, AND A SQUAMOUS CELL FIRSOFORM IS FOUND IN LINE, TAX THE COLLAGEN XILDNEY, AND A SQUAMOUS CELL FIRSOFORM CELL LINE.

C. CRACILOMA CELL LINE.

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C. CRACILOMA CELL COLL
 PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).
 182
 429
 472
 258 GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVALITFASQPKTIMSILS 317
 EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY SIMILARITY).
 144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----KD
 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE
 183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
 430 LNE--LGSKKDGERHAFILODA-KALOQIFEHMLDVSKL-----TDTICG-----V
 PTM: GLYCOŚYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
 CAIC_HUMAN STANDARD; PRT; 3063 AA. 099715; 099716; 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) collagen alpha 1(XII) chain precursor. COL12A1.
 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-
 299 MND----GLSFISSSVII 312
 : | | : | | | 531 VGDPTSQHGKEFLVEDVII 549
 CA1C_HUMAN
 318
 243
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 SMART: SHOULE: PSSOUSE: WRFA: 4.
PROSITE: PSSOUSE: WRFA: 4.
Extracellular matrix: Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
 WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NC1).
TO CHONDROITH SULFATE (POTENTIAL).
TO CHONDROITH SULFATE (POTENTIAL).
TO CHONDROITH SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: CONTAINS 4 VWFA DOMAINS.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
 HYDROXYLATION (BY SIMILARITY)
HYDROXYLATION (BY SIMILARITY)
HYDROXYLATION (BY SIMILARITY)
 WITH 1 IMPERFECTION.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
 TRIPLE-HELICAL REGION (COL2)
 COLLAGEN ALPHA 1(XII) CHAIN.
 FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
 FIBRONECTIN TYPE-III 18
 NONHELICAL REGION (NC3)
 FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 10
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 13
FIBRONECTIN TYPE-III 14
FIBRONECTIN TYPE-III 14
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 16
 FIBRONECTIN TYPE-III 1.
 2.
 FIBRONECTIN TYPE-III
 MINI; LAUSZO, IPRO0087; Collagen.
Interpro; IPR003961; FN III.
Interpro; IPR003962; FN III.
Interpro; IPR003129; TSPN.
Interpro; IPR002129; TSPN.
Interpro; IPR002135; WWRA.
Interpro; IPR002135; WWRA.
Interpro; IPR002105; TSPN.
Interpro; IPR00210; TSPN.
IPRN; PR00041; FN; 4.
PRINTS; PR00043; WWRADDMAIN.
 VWFA 4
 VWFA
 EMBL; U73778; AAC51244.1; -. EMBL; U73779; AAD40483.1; -.
 SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
 903
998
1085
1178
1371
 SMART; SM00060; FN3; 17
 1473
1564
1652
1751
 1842
1932
2023
2114
22202
 2746
2898
 3063
798
889
981
864
 2496
 3044
 P02751; 1TTF.
 2115
2203
2323
2451
2747
 2899
 1565
1654
1752
1843
1933
2024
 120320;
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RECEPTORS.
 DOMAIN
 THE HELET LETERAL AND DEATH AND DEAT
 18;
 370 PWTAGSRQHALSVG------PQTTTLSVRDLSADTEY------QISVSAMKGWTS 412
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 EDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 212
 255 DEV----EIPARELRNVGVEVFSLGIKAADAKELKQIASTPSLNHVFNVAN-FDAIVDIQ 309
 213 HSILKKSCI-----EILAAE-----PSTICAGESFQVVVRGN------GFR---- 247
 310 NEIISQVCSGVDEQLGELVSGEEVVEPPSNLIAMEVSSKYVKLNWNPSPSPVTGYKVILT 369
 -----HARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
 REQIRQGLEELQKV-LPGGDTYMHEGFERASEQIYYEN---RQGYRTASVIIALTDGELH 154
 Gaps
 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFI--SPQLRMSFIVFSTRGTTLMKLTE--D 98
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 74;
 .;
В
 (POTENTIAL)
 6.8%; Score 131; DB 1; Length 3063; 22.1%; Pred. No. 0.032; ive 71; Mismatches 116; Indels 74
 TISSUE-Embryo;
MEDLINE-91185668: PubMed-8444186;
Waelchli C., Trueb J., Kessler B., Winterhalter K.H., Trueb lacomplete primary structure of chicken collagen XIV.";
Eur. J. Biochem. 212:483-490(1993).
 SIMILARITY).
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 SIMILARITY)
 SIMILARITY)
 ISOFORM).
 75FEA78FA8E48293 CRC64;
HYDROXYLATION (BY SIMILA HYDROXYLATION (BY SIM
 01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XIV) chain precursor (Undulin).
 SEPISIMEKTQPMKVQVECSRG--VDIKADIVFLV 445
 300 NDGLSFI-SSSVIITTTHCSDGSILAIALLILFLL 333
 PRT; 1888 AA
 ...
 [2]
SEQUENCE OF 402-1549 FROM N.A.
MEDLINE-92339443; PubMed-1339349;
 333189
 Query Match
Best Local Similarity 22.1%
Matches 74; Conservative
 STANDARD;
 Gallus gallus (Chicken).
 2971
2997
33000
33000
3029
3029
700
700
11763
1188
 1763 1763
2206 2206
2528 2528
2679 2679
25 1188
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 3000
3000
30014
3023
3026
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700
 CAIE_CHICK
P32018;
 MOD_RES
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 413
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Trueb D., Trueb B.;

M. Trueb J., Trueb B.;

M. Trueb J., Trueb B.;

M. Miller-92920705; Pubmed-1053046;

M. Miller-92920706;
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EGF-LIKE 40.
SEA 1.
SEF 1.
SEF-LIKE 41.
EGF-LIKE 42.
EGF-LIKE 44.
EGF-LIKE 44, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 45.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                 PROSITE; PS00010; ASX_HYDROXYL; 28.
PROSITE; PS00021: EGF_1; 1.
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS0124; EGA; 2.
PROSITE; PS50244; EGA; 2.
Hypothetical protein; EGF-like domain; Repeat; Transmembrane.
                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1 (PARTIAL).
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 9.
EGF-LIKE 9.
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EGF-LIKE 15.
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EGF-LIKE 19.
EGF-LIKE 21.
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EGF-LIKE 24.
EGF-LIKE 27.
EGF-LIKE 26.
EGF-LIKE 27.
EGF-LIKE 27.
EGF-LIKE 27.
EGF-LIKE 37.
EGF-LIKE 37.
EGF-LIKE 31.
EGF-LIKE 33.
EGF-LIKE 33.
EGF-LIKE 33.
EGF-LIKE 33.
EGF-LIKE 34.
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EGF-LIKE
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EGF-LIKE
EGF-LIKE
                     Pfam; PF00008; EGF: 30.
Pfam; PF01090; SEA; 2.
Pfam; PF00092; vwa; 1.
SMART; SM00109; EGF_LA; 1.
SMART; SM00001; EGF_LIke; 38.
SMART; SM00320; SEA; 2.
EGF_Ca
                                                                                                                                                                                             InterPro; IPR001881;
InterPro; IPR000082;
         InterPro; IPR000082;
InterPro; IPR002035;
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                                                                                                                                 12;
                                                                                                                                                                                                                                                                              1213 DELITEVCETASATCPLVFKDGDKLA-----GFKMMEMFGLVEKEFSAIDGVSMEPGTF 1266
                                                                                                                                                                                                  DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 212
                                                                                                                                                                                                                                                               213 HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF 272
                                                                                                                                                                                      98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                 26; Gaps
                                                                                                                                                 DLYFILDKSGSV-LHHWNEIYYEVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 97
                                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LIKKED (GLCNAC. .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
MM; 39915BB9F46DD873 CRC64;
                                                                                                              6.8%; Score 130; DB 1; Length 1888;
25.0%; Pred. No. 0.021;
tive 44; Mismatches 116; Indels 20
                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
16-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein T20G5.3 in chromosome III (Fragment).
T20G5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRIGTOL N2;
BEAKS M., Smith A.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: CONTAINS 45 EGF-LIKE DOMAINS.
-: SIMILARITY: CONTAINS 2 SEA DOMAINS.
-: SIMILARITY: CONTAINS 1 VWFA DOMAIN.
    VWFA 2.
NOWHELICAL REGION (NC4).
TRIPLE-HELICAL REGION 1.
TRIPLE-HELICAL REGION 2.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                    PRT; 3051 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mormbep; T20G5.3; CE00478.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z30423; CAA83007.1; -. PIR; S42373; S42373.
                                                                                       202666
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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1468
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1786
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62;
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P34576;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                             PRINTS; PRO0453; "WFADOMAIN.
SMART; SM00181; EGF; 1.
SMART; SM00327; WWA; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50234; WWFA; 2.
PROSITE; PS50234; WWFA; 2.
EGF-like domain; Signal; Glycoprotein; Cartilage; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 ENRQGYRTAS--VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                        82 FIV---FSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 GLVQYSSSVRQEFPLGREHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSF 366
                                                                                                                                                                                                                                                                                                                                                                                                                  264 VCSGGGGS-----SATDLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQV 314
                                                                                                                                                                                                                                                                                                                                                                                                     24 ICAGQGGRREDGGPACYGGFDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 ADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASEPVAEHYFYTAD-FKTINQIGKKLQKKICVE---EDP---CACESLVKFQAKVEG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAIC_NOTVI STANDARD; PRT; 929 AA.

Q91145;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Nociphthalmus viridescens (Eastern newt) (Triturus viridescens).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 TVSSGARPGAQKVGIVFTDGRSQD----YINDAAKKAKDLGFKMFAVGVGNAVEDELREI
                                                                                                                                                                                                                                                                                         . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                   Score 120.5; DB 1; Length 496;
Pred. No. 0.023;
7; Mismatches 95; Indels 45;
                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
2D880A8114C7940F CRC64;
                                                                                                                                                                                                                                                 CARTILAGE MATRIX PROTEIN
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                   EGF-LIKE.
                                              37;
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                                                                                                                                             InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                         452
53700
                                                                                                                                                       IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                         60; Conservative
                                                                                                                                                              Pfam; PF00008; EGF; 1.
Pfam; PF00092; vwa; 2.
                                                                                                                                                                                                                                                                                                                                         265
496 AA;
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                                                                                                                              P05099; 1AQ5.
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223
264
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MIM; 115437
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LUCALLIZED IN THE FEKIFIBKILLIAN PARIKIA (BI SIRLHMATIII). COLUL FLAII

A DEVELOPMENTAL ROLE IN REGENERATION.

C -1- SUBUNIT: TRIMER OF IDENTICAL CHAINS BACH CONTAINING 190 kDa OF

NOWTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).

C -1- DEVELOPMENTAL STAGE: EXPRESSION STARTS AT 3 DAYS AFTER AMPUTATION

IN CELLS OF THE BASAL LAYER OF THE WOUND EPITHELLIU. AT DAY 10,

THE DISTAL MESSENCHYME CELLS. AT MID-BUD AND LAYE-BUD BLASTEMA

STAGES, WOUND EPITHELLIUM EXPRESSION HAS DECREASED, WHEREAS THE

STAGES, WOUND EPITHELLIUM STREPSSION HAS DECREASED, WHEREAS THE

STAGES, WOUND EPITHELLIUM STREPSSION HAS DECREASED, WHEREAS THE

C STREDENCY TOWARD DISTAL REGIONALIZATION. CONDENSING CARTILLES SHOWS

NO SIGNAL. FINALLY, AT THE LAYE DIGIT STAGE, EXPRESSION BECOMES

NO SIGNAL. PITHEL-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT

C -1- PTM: THE TRIPLARITY).

C -1- PTM: THE TRIPLARITY).

C -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPREATING

C -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING

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C -1- THE CALLY APPENT.
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TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
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-!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
-!- SIMILARITY: CONTAINS 2 VWFA DOMAINS.
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
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FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
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2 (bases 1 to 1414)
Bradley.K.A., Mogridge,J., Mourez,M., Collier,R.J. and Young,J.A.T.
Direct Submission
Submitted (19-SEP-2001) Department of Oncology, University of
Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1414)

Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.

Adeniification of the cellular receptor for anthrax toxin

Nature 414 (6860), 225-229 (2001)
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Copyright (c) 1993 - 2000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                Submitted (16-JUN-2000) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, 3 (bases 1 to 5540)
St. Croix, B., Vogelstein, B. and Kinzler, K.W.
Direct Submission
Submitted (09-MAY-2001) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, 5equence update by submitter
On May 9, 2001 this sequence version replaced gi:9857405.
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/product="tumor_endothelial_marker 8 precursor"
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St. Croix, B., Vogelstein, B. and Kinzler, K.W. Direct Submission Submitted (16-JUN-2000) Johns Hopkins Oncolo
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Pred. No. 2.9e-306;
0; Mismatches 2;
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/db_xxef="taxon:9606"
/chromosome="4"
1. .5540
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/gene="TEM8"
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Homo sapiens, Similar to tumor endothelial marker 8, clone MGC:19967 IMAGE:4563020, mRNA, complete cds.

BC012074
BC012074
BC012074.1 GI:15082332
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tahnase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens teratocarcinoma cell_line:NT2
clone_lib:NT2RP2 clone:NT2RP2005000.
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DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Letticia Hsiao, Martin Krzywinski, Reta Rutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvands Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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/product="5imilar to tumor endothelial marker 8"
/product="5imilar to tumor endothelial marker 8"
/db_xref="61:1508233"
/db_xre
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                      Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/lab_host="DH10B-R"
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Pred. No. 8.7e-269;
0; Mismatches 1;
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/db_xref="taxon:9606"
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113. .1114
                                                                                                                                         Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Carson-Walter,E.B., Watkins,D.N., Nanda,A., Vogelstein,B., Kinzler,K.W. and St. Croix,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carson Walter, E.B., Vogelstein, B., Kinzler, K.W. and St. Croix, B. Direct Submitted (101-MAY-2001) Oncology, Johns Hopkins University, 1650 orleans Street, Baltimore, MD 21231, USA
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/organism="Mus musculus"
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[Sogai,T. and Otsuki,T.

[Sogai,T. and Otsuki,T.

[Sogai,T. and Otsuki,T.

[Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@khi.co.jp, Tel:81-438-52-3951, Rax:81-438-52-3952)

[MEDO human CDNA sequencing project supported by Ministry of

International Trade and Industry of Japan; CDNA full insert

Sequencing: Research Association for Biotechnology; CDNA library

CONSILUCTION, 5' & 3'-end one pass sequencing and clone selection:

Helix Research Institute (Supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="Baa91707.1"
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/translation="MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEG
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/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="cloning vector: pME18SFL3; mRNA from NT2 in precursor cells after 2-weeks retinoic acid (RA) induction "
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Pred. No. 1.2e-225;
0; Mismatches 5;
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/note="unnamed protein product"
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/db_xref="taxon:9606"
/clone="NT2RP2005000"
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Best Local Similarity 99.3%;
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/note="unnamed
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Pred. No. 1e-215;
); Mismatches 136; Indels 0;
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1329 c 1235 g 1250
                                                                                                               /product="tumor
1228, .1293
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355. .1959
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87.38;
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/gene="Tem8"
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                                                                                                                          misc_feature
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Homo sapiens CDNA: FLJ21776 fis, clone HEP00171.

Homo sapiens CDNA: FLJ21776 fis, clone HEP00171.

Homo capping; fis (full insert sequence).

Homo sapiens, hepatoma cell_line: HepG2 cDNA to mRNA, clone_lib: HEP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1070
                                                                                                                                                                             996
agttggcatgaaagctgcactccaggtcagcatgaacgatggcctctctttatctccag
                                                                                                                                                                                      tgagaagcccttttctgtggaagacacttatttactgtgtccagcgcctatcttaaaaga
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/cell_type="hepdcoma"
/clone_lib="HEP"
/note="cloning vector ph
323. .1147
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Submitted (124-007-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-22-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full Insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- 6 3'-end one pass sequencing: RNB, HRI, and Blotechnology Center, National Institute of Technology and Evaluation; clone selection for full Insert sequencing: RAB and
Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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459 t
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Pred. No. 7.7e-57;
0; Mismatches 377;
                                                                                                                                          Isogai, T., Otsuki, T. and Sugiyama, T. Direct Submission
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614 c 517 g 4
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I (sites)
Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiquchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
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Catarrhini; Hominidae;
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to mRNA, clone_lib:TESTI2
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                                                                                                                                                                                              Score 542.8; DB 9;
Pred. No. 4.2e-133;
0; Mismatches 2;
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Mammalia; Eutheria; Primates;
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Homo sapiens testis cDNA
clone:TEST12001671.
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99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Center Center Center Code: BCM-HGSC.
Center code: BCM-HGSC.
Web site: http://www.hgsc.bcm.tmc.edu.
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Submitted (15-AUG-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                           963 aagaagttggcatgaaagctgcactccaggtcagcatgaacgatggcctcttttatct 1022
                                                                                                                                                                  843 gacatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcacac 902
                                                                                                                                                                                             860 TIGATGAAAAGCCAACCAGTATCGACAATAATTCCATGAATTGCCCTGGGCCAAAACTAG 919
                                                                                                                                                                                                                                                                                                                                                                                  920 AAAAACCIGGAGAGAGTACTCTATTGAAGTCAGCTTGAACAAAGGCAAAAACATTCTTCA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
723 ctctgcaaggcatcatccactcaattttgaagaagtcctgcatcgaaattctagcagctg
                                    783 aaccatccaccatatgtgcaggagtcatttcaagttgtcgtgaggaggaaacggcttcc
                                                                                                                         740 AGGUTICCICIGAGIGIGIAGAGAGCCIACCAIGIGGITATICAIGGAAAIGGCITIC
                                                                                                                                                                                                                                                           tcaatgagaagcccttttctgtggaagacacttatttactgtgtccagcgcctatcttaa
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1297)
Strausberg, R.
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Homo sapiens, clone IMAGE:4705862, mRNA, partial cds.
EC012475
EC012475.1 GI:15214683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIH-MGC Project URL: http://mgc.nci.nih.gov
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<1. .295</pre>
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/tissue_type="Breast, marming"
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/lab_host="DH108"
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To Cases 1 to 2026)

S Isogal, T., Otsuki, T. and Sugiyama, T.

Reboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Genomics Chirico, jp, Tel: 81-438-52-3951, Fax:81-438-52-3952)

RED Munan CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA illivary

Research Association for Biotechnology (RAB); CDNA illivary

Construction: Helix Research Institute (HRI) (supported by Japan Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- s 3-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and HRI, and Biotechnology Center, National Institute of Rechnology and Evaluation; clone selection for full insert sequencing: RAB and
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Ninomiya, K., Wagatsuma, M., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kodaira, H., Furuya, T., Takahashi, M., Tanikawa, M., Yamazaki, M.,
Kamihara, K., Ratsuta, N., Sato, K., Tanikawa, M., Yamazuki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Sugano, S.,
NEDO human CDNA sequencing project
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/translation="FOVVRGNGFRHARNUDSFLCSFKINDSVTLNEKPFSVEDTYLL
/translation="FOVVRNDGIJFFISSSVIITTTQGSLHKIASGPTTAACME"
333 c
333 c
276 g 323 t
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oligo capping; fis (full insert sequence).
Homo sapiens synoviocytes from rtheumatioid arthritis (HS-RA) cDNN
to mRNN, clone_lib:HSYRA2 clone:HSYRA2001476.
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA FLJ31074 fis, clone HSYRA2001476.
AK055636
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                                                                                                                                                                                                                                                                                                                      Score 236; DB 9; I
Pred. No. 1.2e-51;
0; Mismatches 5;
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98.0%;
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 134)
1 (Bases I to 134)
1 (Bases I to 134)
1 (Bases I to 134)
Maxwell, S.A. and Davis, G.E.
Differential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling
1 Cell. Sci. 114 (Pt 15), 2755-2773 (2001)
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POPPOTRWYTPLKGGIRKMEVRWCYDFKGYDFVANNAVKIPEETEEPIRFRPPRPTH
297 c 377 g 326 t
                                                                                                                                                                                                                            PRI 22-JAN-2002
                                                                                                                                                                                                                            AY040326 1343 bp mRNA linear PRI 22-JAN-2003
Homo sapiens capillary morphogenesis protein-2 mRNA, complete cds.
AY040326.1 GI:15418998
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/note="CMG-2; contains a von Willebrand factor A domain;
regulated during endothelial cell morphogenesis; targets
to the endoplasmic reticulum"
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Submitted (14-JUN-2001) Pathology, Texas A&M University System
Health Science Center, 208 Reynolds Medical Building, College
Station, TX 77843-114, USA
Location/Qualifiers
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Pred. No. 3.9e-44;
0; Mismatches 257;
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/chromosome="4"
                                    677
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Davis, G.E. and Bell, S.E.
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14.7%;
59.0%;
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Best Local Similarity 59.0°
Matches 378; Conservative
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/clone="HSYRA2001476"
/cell_type="synoviocytes from rtheumatioid arthritis
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Homo sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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321 GAAATTTATAATTTCGTACAGCAACTTGCGGAGAGATTTGTGAGCCCTGAAATGAGATTA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       735 GICAAAGGIGGATIICAGGCICTIAAAGGAATAATIC 775
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HTG; HTGS_PHASE0.
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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10188 10287: gap of

10288 11042: contig of 755 by -

11043 11142: gap of

11143 11910: contig of 768 bp in length

111911 12010: gap of

12011 12010: gap of

12018 12857: gap of

12018 12857: gap of

12018 12857: gap of

12018 12857: gap of

12018 1287: gap of

12018 13619: contig of 762 bp in length

12018 13619: contig of 762 bp in length
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
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21337: contig of 744 bp in length
21437: gap of 100 bp
22202: contig of 765 bp in length
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20493: contig of 751 bp in length
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5899: cont
5999: gap of
6764: cont
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4176: cor
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gap of 100 bp contig of 761 bp .

of 100 bp of 100 bp ad0: contig of 756 bp in lens.

40: gap of 100 bp ad0: contig of 753 bp in length appoint app of 100 bp ad0: contig of 753 bp in length appoint app of 100 bp ad0: contig of 757 bp in length appoint appoint app of 100 bp ad0: contig of 755 bp in length appoint app of 100 bp ad0: contig of 755 bp in length appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoint appoin
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glnde, S., Gyotte, M., Graham, L., Grand-Pierre, N., Grand, G., Hados, B., Hadord, A., Horton, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Landers, T., Lehockky, J., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurt, A., Mickernan, K., Mcheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Peterre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigillo, J., Testayers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC025010 81017 bp DNA linear HTG 13-JUL-2000 HOMO sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE SAMPLING.
AC025010.1 GI:7145054 HTG; HTGS_PHASEO.
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1 (bases 1 to 81017)

Birran, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 4, clone RP11-85D17
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                                                                                                                                                                                                                                                                                                                                                                           Score 194.4; DB 2; Length 81017;
Pred. No. 5.7e-40;
0; Mismatches 1; Indels 0;
100 bp
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99.5%;
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Matches 195; Conservative
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* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                      ap of 100 bp in length in contig of 748 bp in length in contig of 747 bp in length in contig of 762 bp in length in contig of 762 bp in length
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7612: con
7712: gap of
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013: gap of 100 bp in 150. 44770: gap of 100 bp 45631: contig of 761 bp in length 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 
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23072: contig of 770 bp ir
3172: gap of 100 bp
23941: contig of 769 bp ir
4041: gap of 100 bp
24799: contig of 758 bp in
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100 bp
g of 755 bp in length
100 bp
g of 758 bp in length
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18767: contig of 767 bp in length
18867: gap of 100 bp
19742: gap of 100 bp
19742: gap of 100 bp
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of 746 bp in length
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contig of

14493

14593: gap of 15348: contig

contig of

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gap of gap of

5349 15448: 16306:

contig con 17900:

17901 18000: gap of 18001 18767: con

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G. Consortium (LLNL)
DNA Sequencing by: Sequencing froup at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
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/db_xref="taxon:10090"
/db_MdE:3484366"
/tissue_type="Hammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
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construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2557)
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Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/XLNL at: http://lmage.llnl.gov series: IRAK Plate: 7 Row: e Column: 5 Series: IRAK Plate: 7 Row: e Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Mus musculus, clone IMAGE:3484366, mRNA, partial cds.
ECU03908
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100.0%; Pred. No. 6.3e-19;
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Matches 113; Conservative 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1009794"
/clone_lib="PLACE1"
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The Common CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library
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Isogai, T. and Otsuki, T.
Direct Submission
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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clone:PLACE1009794.
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20 51719; gap of 100 bp 52473; contig of 754 bp in length 53247; contig of 754 bp in length 100 bp 53327; contig of 754 bp in length 53327; contig of 754 bp in length 100 bp 54198; contig of 771 bp in length 100 bp 55054; contig of 756 bp in length 100 bp 55054; contig of 767 bp in length 100 bp 550514; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 b
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PNKKWPTVDASYYGGRGVGGIKRMEVRWGDKGSTEEGARLEKAKNAVVMVPEEEIPIP
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/protein_id="AAH03908.1"
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13-JUL-2000 (Rel. 64, Last updated, Version 3)
                                  /note="Vector: pCMV-SPORT6"
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"The sequence of Homo sapiens clone";
Unpublished.
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Sequencing Center, Washington University School of Medicine, 4444 park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                        On Jul 12, 2000 this sequence version replaced gi:8810547
                                                                                                                             Sequencing vector: Navivatistics
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 141001 bases at least 040
Consensus quality: 146066 bases at least 020
Consensus quality: 149318 bases at least 020
Insert size: 178000; agarose-fp
Insert size: 178000; agarose-fp
Ouality coverage: 3.25 in 020 bases; sum-of-contigs
                                                                   Center: Washington University Genome Sequencing Center
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/organism="Homo saplens"
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1253 aacacagcccgtgcaacgtattttatacaatgctctgaaaatcatagtctcaatctagac 1312 Gaps ö Length 162448; 74247. . 20310 7017. . 205752 27017. . 28752 70016. . assembly_name:Contig33" 20853. . 30683 7001e. . assembly_name:Contig34" 30784. . 32471. 7001e. . assembly_name:Contig35 clone_end:T7 vector_side:right" 32572. . 34605 7016. . 37543 /note="assembly_name:Contig27 clone_end:SP6 vector_side:left"
16339...17828
1700te="assembly_name:Contig28" Ouery Match 4.4%; Score 62; DB 30; Length 16 Best Local Similarity 55.0%; Pred. No. 0.00012; Matches 122; Conservative 0; Mismatches 100; Indels /note="assembly_name:Contig29" 19941. :1917 /note="assembly_name:Contig30" 22018. :24146 /note="assembly_name:Contig31" 24247. :26916 /note="assembly_name:Contig37" 37644. .40004 /note="assembly_name:Contig38" misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature ò g g q ò

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Search completed: August 9, 2002, 00:23:20 Job time: 12457 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2002, 10:35:58 ; Search time 98.32 Seconds (Without alignments) 388.682 Million cell updates/sec August Run on:

US-09-970-076-10 1131 1 MSFIVFSTRGTTLMKLTEDR......sTSGFKEGNSHPCLPARPHT 218 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

528882 Total number of hits satisfying chosen parameters:

528882 seqs, 175299045 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

1: /cgn2_6/ptcdata/2/paa_VCT_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa_VUS06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa_VUS07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa_VUS09_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa_VUS09_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa_VUS10_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa_VUS10_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 11706, A			22	24,	Sequence 18, Appl	Sequence 187, App	• •	Sequence 20, Appl	Sequence 1823, Ap	_		12, 4	10,	14,	16,	66	σ		10,	312	Sequence 8, Appli	4	43,	Sequence 257, App	61, 7
QI	US-09-629-469A-11706	US-10-038-307-26	US-10-038-307-2	US-10-038-307-22	US-10-038-307-24	US-10-038-307-18	PCT-US02-08253-187	PCT-US02-08253-232	US-10-038-307-20	US-60-389-987-1823	PCT-US02-08253-194	PCT-US02-08253-301	US-10-038-307-12	US-10-038-307-10	US-10-038-307-14	US-10-038-307-16	US-10-047-542-99	US-10-104-047-2639	US-10-038-307-6	US-60-373-595-10	US-10-125-540-312	US-10-038-307-8	US-10-038-307-4	US-09-592-617A-43	PCT-US02-08253-257	PCT-US02-19669-61
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% Query Match	100.0	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	84.9	84.9	83.6	83.6	83.6	83.6	62.2	44.7	44.7	44.7	44.7	43.8	36.7	8.6	6.3	9,3
Score	1131	996	996	996	996	996	996	996	996	996	096	096	945	945	945	945	704	206	206	206	505	495	415	111	105.5	105.5
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Length 218; Indels

Query Match 100.0%; Score 1131; DB 5; Best Local Similarity 100.0%; Pred. No. 5.6e-106; Matches 218; Conservative 0; Mismatches 0;

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ALIGNMENTS

RESULT 1 US-09-629-469A-11706 Sequence 11706, Application US/09629469A Sequence 11706, Application US/09629469A Sequence 11706, Application US/09629469A APPLICANT: ISOGAI, TAKAO APPLICANT: SOGAI, TAKAO APPLICANT: SIGHKAWA, TETSUO APPLICANT: SIGHKAWA, TETSUI APPLICANT: SIGHKAWA, TETSUI APPLICANT: WARANATSU, AI APPLICANT: WARANATSU, AI APPLICANT: WARANATSU, AI APPLICANT: WARANATSU, PILMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND FILE REFERENCE: 2000-07-28 PRIOR PELICATION NUMBER: US/09/629,469A CURRENT APPLICATION NUMBER: US/09/629,469A PRIOR FILING DATE: 1999-07-29 PRIOR PELICATION NUMBER: UP 1999-300253 PRIOR PELICATION NUMBER: UP 2000-118776 PRIOR PELICATION NUMBER: UP 2000-183767 PRIOR PELICATION NUMBER: UP 2000-183767 PRIOR PELICATION NUMBER: UP 2000-183767 PRIOR PELICATION NUMBER: GO/183,322 PRIOR PELICATION NUMBER: 60/183,322
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Homo sapiens
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; ORGANISM: Hc
US-10-038-307-2
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; Sequence 2, Application US/10038307
; Sequence 2, Application US/10038307
; GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'REFF
APPLICANT: Engin OSKANNAK
; APPLICANT: Dudith J. HEALEX
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; TILE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; TILE REFRENCE: 7853-253-999
; CURRENT FILING DATE: 202-06-28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SSOFTWARE: PASTSEQ for Windows Version 4.0
; SED ID NO 2
; LENGTH: 333
; TYPE: PRT
                                                                                                                                                                                                                                                                  Sequence 26, Application US/10038307
| Sequence 26, Application US/10038307
| Sequence 26, Application
| Septence 26, Application
| APPLICANT: James B. ROTTMAN
| APPLICANT: Engin OZKAYNAK
| APPLICANT: Engin OZKAYNAK
| APPLICANT: Mile 17, HEALEY
| TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
| TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
| TITLE OF INVENTION: TANGO 197 and Tango 216 Compositions and Methods
| TITLE OF INVENTION: TANGO 197 and Tango 216 Compositions and Methods
| TITLE OF INVENTION NUMBER: US/10/038, 307 |
| CURRENT FILING DATE: 2002-06-28 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH 328 |
| LENGTH 328 |
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                                         1 MSFIVESTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                        PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF
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Pred. No. 4.2e-89;
2; Mismatches 0; Indels
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                                                                                                                                                                          Query Match 85.4%;
Best Local Similarity 98.9%;
Matches 188; Conservative
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US-10-038-307-26
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US-10-038-307-2
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US-10-038-307-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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                                                                                 Sequence 22, Application US/10038307

Sequence 22, Application US/10038307

GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Horiesa L. O'KEFF
APPLICANT: Engin OZKANANA
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
TITLE REFERENCE: 7853-253-99
CURRENT FILIGATION NUMBER: US/10/038,307
CURRENT FILIGATION NUMBER: US/10/038,307
CURRENT FILIGATION OF 202-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFIVESTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
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Length 333
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Pred. No. 4.4e-89;
2; Mismatches 0;
 Score 966; DB 6;
Pred. No. 4.2e-89;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: James B. ROTTMAN APPLICANT: Theresa L. O'KEEFE
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98.9%;
       85.4%;
98.9%;
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                       Best Local Similarity 98.9
Matches 188; Conservative
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ORGANISM: Homo sapiens
US-10-038-307-22
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Matches 188; Conserv
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260 KINDSVTLNE 269
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-USO2-08253-187
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ORGANISM: Homo sapiens
                             260 KINDSVTLNE 269
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      181 KINDSVTLSK 190
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PCT-US02-08253-232
                                                                                            PCT-US02-08253-187
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LENGTH: 564
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APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ 1D NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
ITILE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
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                                                                                                                                                                                                                                     Score 966; DB 6; Length 345;
Pred. No. 4.4e-89;
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SOFTWARE: FastSEQ for Windows Version 4.0
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98.9%;
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Best Local Similarity
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                                                                                                                       SEQ ID NO 24
LENGTH: 345
TYPE: PRT
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LENGTH: 551
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Dy 181 KINDSVILME 269

RESULT 7. PCT-0260-0253-187

Sequence 1877. Application PC/TUS0208233

Sequence 1877. Application PC/TUS0208233

Sequence 1877. Application PC/TUS0208233

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Gibson, Bradford
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US-60-389-987-1823
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Best Local Similarity
Matches 187; Conserv
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260 KINDSVTLNE 269
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US-10-038-307-20
Sequence 20. Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-2599
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 564
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Pred. No. 8.7e-89;
. ....has 0; Indels
                                                    Length 564;
                                                                              Indels
                                                   Score 966; DB 1;
Pred. No. 8.7e-89;
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Sequence 1823, Application US/60389987

GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Fahy, Eoin D.

APPLICANT: Zhang, Bing
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98.9%;
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98.9%;
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Matches 188; Conserva
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260 KINDSVTLNE 269
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                                                                      188; Conservation
                 PCT-US02-08253-232
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                                                                          Best Local
Matches 18
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APPLICANT: TAYLOL, STEVEN W.
APPLICANT: TAYLOL, STEVEN W.
APPLICANT: TAYLOL BAILE E.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 1DENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 2002-06-17
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1823
LENGTH: 564
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; Sequence 144, Application.
GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PLILICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR PILICATION NUMBER: 66/308,829
PRIOR FILING DATE: 2001-08-01
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Pred. No. 8.7e-89;
2; Mismatches 0; Indels
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llarity 98.4%; Pred. No. 3.5e-88;
Conservative 2; Mismatches 1; Indels
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SOFWMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 194
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Best Local Similarity 98.9%;
Matches 188; Conservative
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11 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 130
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APPLICANT: Theresa L. O'KEFFE
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastsEQ for Windows Version 4.0
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                                                                                                           Length 534;
                                                                                                                                            0; Indels
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Pred. No. 1.1e-86;
2; Mismatches 0;
                                                                                                         Score 945; DB 6;
Pred. No. 1.1e-86;
                                                                                                                                            2; Mismatches
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Best Local Similarity 97.9%;
Matches 186; Conservative
                                                                                                         83.68;
                                                                                                         Query Match 83.6
Best Local Similarity 97.9
Matches 186; Conservative
 ; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-12
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ORGANISM: Homo sapiens
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Sequence 12, Application US/10038307
Sequence 12, Application US/10038307
Sequence 12, Application US/10038307
Sequence 12, Application US/10038307
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEFE
APPLICANT: Theresa U. O'KEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-233-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 562;
                                                                                                                                                                                                                                        Sequence 301, Application PC/TUS0208253
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Worlstein, Bert
APPLICANT: Winzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00179
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-11
PRIOR PELICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 3001-08-01
NUMBER OF SED ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 562
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258 KINDSVTLNE 267
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Matches 187; Conserv
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ORGANISM: Mouse
                                                                                                                                                                                                            RESULT 12
PCT-US02-08253-301
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Query Match

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Gaps

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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Houdith J. HEALEY
TITLE OF INVANION: Tango 197 and Tango 216 Compositions and Methods
FILE REPERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 543
FYPE: PRT
CENTRAL 543
FYPE: PRT
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83.6%; Score 945; DB 6; Length 54:
Best Local Similarity 97.9%; Pred. No. 1.1e-86;
Matches 186; Conservative 2; Mismatches 0; Indels
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258 KINDSVTLNE 267
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Search completed: August 9, 2002, 10:35:59 Job time: 357 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:35:57; Search time 98.32 Seconds Run on:

(without alignments) 593.720 Million cell updates/sec

8-920-026-60-sn

1728 1 MATAERRALGIGFQWLSLAT......TTHCSLHKIASGPTTAACME Perfect score: Sequence:

333

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

528882 seqs, 175299045 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pending_Patents_AA_New:*

1: /cgnl2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgnl2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgnl2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

4: /cgnl2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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7: /cgnl2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result	5	Query	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Ę	í.	
. ON	score	March	Match Length UB	9 1	TD	Description
	1728	100.0	333	9	US-10-038-307-2	Sequence 2, Appli
7	1728	100.0	564	ø	US-10-038-307-20	20,
m	1718	99.4	345	9	US-10-038-307-24	Sequence 24, Appl
4	1713.5	99.5	342	9	US-10-038-307-22	22,
ഗ	1650.5	95.5	551	9	US-10-038-307-18	18,
9	1649	95.4	564	-	PCT-US02-08253-187	187,
7	1649	95.4	564	ч	PCT-US02-08253-232	
æ	1649	95.4	564	7	US-60-389-987-1823	1823,
თ	1636	94.7	328	9	US-10-038-307-26	
10	1628	94.2	543	9	US-10-038-307-14	14
11	1628	94.2	543	ø	US-10-038-307-16	16,
12	1618	93.6	543	9	US-10-038-307-10	10,
13	1553	89.9	562	-	PCT-US02-08253-194	194,
14	1553	89.9	562	-	PCT-US02-08253-301	301,
15	1487	86.1	534	9	US-10-038-307-12	12, A
16	996	55.9	218	S	US-09-629-469A-11706	117
17	903	52.3	538	9		
18	800.5	46.3	488	9	US-10-104-047-2639	Sequence 2639, Ap
19	800.5	46.3	488	9	US-10-038-307-6	
. 50	800.5	46.3	488	7	US-60-373-595-10	10,
21	785.5	45.5	287	9	US-10-125-540-312	312
22	771	44.6	487	9	US-10-038-307-8	8, 7
23	699	38.7	381	9	US-10-038-307-4	4
24	145.5	8.4	1152	'n	US-09-592-617A-43	43,
25	138.5	8.0	1163	~	PCT-US02-10824-116	116,
26	138.5	8.0	1163	7	US-60-369-452-33	33,

Sequence 22380, A Sequence 1, Appli	,	Sequence 257, App	Sequence 61, Appl	Sequence 63, Appl	Sequence 61, Appl	Sequence 63, Appl	Sequence 5866, Ap	Sequence 2, Appli	Sequence 3, Appl1	Sequence 59, Appl	Seguence 4, Appli	Sequence 1591, Ap	Sequence 28757, A	Seguence 34, Appl	Sequence 294, App	Sequence 294, App	Sequence 294, App
US-10-155-881-22380 US-09-805-354-1	US-10-155-881-33525	PCT-US02-08253-257	PCT-US02-19669-61	PCT-US02-19669-63	US-10-177-293-61	US-10-177-293-63	US-60-360-039-5866	US-09-805-354-2	US-09-805-354-3	US-09-592-617A-59	US-10-150-821-4	US-60-389-987-1591	US-10-155-881-28757	US-09-904-920A-34	US-10-121-049-294	US-10-121-050-294	US-10-121-053-294
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7.8	7.6	7.6	7.6	7.6	7.6	9.7	7.4	7.3	7.2	7.0	6.9	9.9	9.9	9.9	9.9	9.9	9.9
134.5	132	131	131	131	131	131	128	125.5	124.5	121.5	118.5	117.5	114	114	114	114	114
27	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James B. FOTTMAN
APPLICANT: Engin OZKAYNAK
APPLICANT: Endith J. HEALEY
TITLE OF INVENTION: Tango 17 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASELEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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                                                                                                                                                                                                                                                                                    Length 333;
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Pred. No. 1.7e-154;
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100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                  Matches 333; Conservative
                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-10-038-307-2
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1
US-10-038-307-2
                                                                                                                                                                                                     LENGTH: 333
TYPE: PRT
                                                                                                                                                                                          SEQ ID NO 2
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DGLSFISSSVIITTHCSLHKIASGPTTAACME 333

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Pred. No. 1.6e-153;

99.78;

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Sequence 20, Application US/10038307

| Sequence 20, Application US/10038307
| GENERAL INFORMATION:
| APPLICANT: James B. ROTTMAN
| APPLICANT: Theresa L. O'KEEFE
| APPLICANT: Engin OZKAYNAK
| APPLICANT: Tango 197 and Tango 216 Compositions and Methods:
| TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods:
| TITLE OF INVENTION: Tango 197 and Tango 216 COMPARENT OF 1853-259-999
| CURRENT PILING DATE: 2002-06-28
| NUMBER OF SEQ ID NOS: 26
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 20
| LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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APPLICANT: Bugin OZKAYNAK
APPLICANT: Bugin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tangle 197 and Tango 216 Compositions and Methods
FILE REPRENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
SOFTWARE: EASTERO FOR MINGOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-10-038-307-20
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LENGTH: 345
 US-10-038-307-20
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                                                                          181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                                 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                    Gaps
                           APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
FILE REFERENCE: 7853-253-999
FURRENT APPLICATION NUMBER: US/10/038,307
CURRENT PILLING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
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Pred. No. 4.2e-153;
0; Mismatches 0;
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           Mismatches
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97.4%;
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Best Local Similarity 97.4
Matches 333; Conservative
Local Similarity 99.7
nes 332; Conservative
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US-10-038-307-22
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US-10-038-307-22
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; TYPE: PRT
; ORGANISM: HOMO S
PCT-US02-08253-187
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SEQ ID NO 187
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GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
TILE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00179
CURRENT FILING DATE: 2002-04-10
PRIOR PPLICATION NUMBER: 60/282,850
PRIOR PPLICATION NUMBER: 60/389,829
PRIOR PPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR PPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
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               301 KAALQVSMNDGLSFISSSVIITTTHCSLHKIASGPTTAACME 342
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Pred. No. 6.9e-147;
2; Mismatches 2; I.
292 KAALQVSMNDGLSFISSSVIITTTHCSLHKIASGPTTAACME
                                                                                                                                           APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Congress Tries of INVENTION: Tango 197 and Tango 216 CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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                                                                                 RESULT 5
US-10-038-307-18
US-10-038-307-18
Sequence 18, Application US/10038307
GENERAL INFORMATION:
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Best Local Similarity 97.3%;
Matches 320; Conservative
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US-10-038-307-18
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GENERAL INFORMATION:

APPLICANT: Carson-Walter, Eleanor

APPLICANT: St. Croix, Brad

APPLICANT: St. Croix, Brad

APPLICANT: Wogelstein, Bert

APPLICANT: Wogelstein, Bert

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: PCT/USO2/08253

CURRENT APPLICATION NUMBER: 60/282,850

PRIOR PELING DATE: 2001-04-10

PRIOR PELING DATE: 2001-04-11

PRIOR FILING DATE: 2001-04-11

PRIOR FILING DATE: 3001-08-01

NUMBER OF SEQ ID NOS: 359

SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                  Pred. No. 9.9e-147; ; Mismatches 0.
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100.0%; Pred. No. 9.9e-147;
ive 0; Mismatches 0;
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100.0%; Pre
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Matches 318; Conservative
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Best Local Similarity
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Sequence 26, Application US/10038307
GENERAL INFORMATION:
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US-10-038-307-14
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                         KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
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                                  HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGALVYCVGV
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Tang, Bing
APPLICANT: Tang, Bing
APPLICANT: Glang, Bing
APPLICANT: Glann, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TILE OF INVENTION: TRAGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SEQ ID NO 1823
SEQ ID NO 1823
LENGTH: 564
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US-60-389-987-1823
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US-60-389-987-1823
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US-10-038-307-26
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100.0%; Pred. No. 7.8e-146;
.ive 0; Mismatches 0;
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Best Local Similarity 99.4%; Pred. No. 9e-145;
Matches 316; Conservative 0; Mismatches 0;
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US-10-038-307-14
Sequence 14, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTNAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
TITLE OF INVENTION: Tango 197 and Tango 216 COM
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TITLE OF INVENTION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Grid OZKAYNAK
APPLICANT: JUGITH J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 (
TITLE OF INVENTION: Tango 197 and Tango 216 (
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
SEQ ID NO 26
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Best Local Similarity 100.0%; P
Matches 316; Conservative 0;
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RESULT 12
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                                             EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                          VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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9
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APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
SUFFRENT FILING DATE: 2002-06-28
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                      HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
                                                                                                                                         KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
MATAERRALG1GFQWLSLATLVL1CAGQGGRREDGGPACYGGFDLYF1LDKSGSVLHHWN
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                                                                                                                                                                                                                                                                                                         US-10-038-307-16; Sequence 16, Application US/10038307; GENERAL INFORMATION:
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Matches 316; Conservative
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US-10-038-307-16
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TILE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1618; DB 6;
Pred. No. 7.8e-144;
                                                           APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Uddith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 (FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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SOFWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 194
LENGTH: 562
Sequence 10, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
                                                                                                                                                                                                                                                                                                                                                                                                                       93.6%;
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                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-038-307-10
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Best Local Similarity
Matches 315; Conserv
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86.1%;
94.5%;
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Best Local Similarity 94.5
Matches 293; Conservative
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Job time: 356 sec
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US-10-038-307-12
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LENGTH: 534
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PCT-USO2-08253-301
SGGUENCE 301, Application PC/TUS0208253
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. CAISON-Walter, Eleanor
APPLICANT: St. CAISON-Walter, Enanct
APPLICANT: St. CAOLA, Brad
APPLICANT: Kinzler, Kenneth
APPLICANT: WOGGIStein, Bert
APPLICANT: WOGGISTEIN, BOTT
ITLE OF INVENTOR: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT PEPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF ESC ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 301
LENGTH: 562
                                              Length 562
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Pred. No. 1.1e-137;
5; Mismatches 7;
                                              Score 1553; DB 1;
Pred. No. 1.1e-137;
5; Mismatches 7;
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ilarity 96.1%;
Conservative
                                               89.9%;
nilarity 96.1%;
Conservative 5
; ORGANISM: Mus musculus PCT-US02-08253-194
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298; Conserv
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                                                Query Match
Best Local Similarity
Matches 298; Conserv
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; ORGANISM: Mouse
PCT-US02-08253-301
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Best Local Si
Matches 298;
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                                               Gaps
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APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
CURRENCE: 7863-239-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT PILING DATE: 2002-06-28
NUMBER OF SEQ 1D NOS: 26
SOFTWARE: FASTESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 534;
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Pred. No. 1.7e-131;
3; Mismatches 8;
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                                                                                                                                                                                                                                                     Sequence 12, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTIMAN
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Search time 507.33 Seconds (without alignments) 231.032 Million cell updates/sec August 9, 2002, 10:44:31 Run on:

US-09-970-076-8 1728 1 MATAERRALGIGFOWLSLAT.....TTHCSLHKIASGPTTAACME 333 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sedneuce:

3502263 segs, 351980561 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/paa/US098_COMB.pep:*/cgn2_6/ptodata/2/paa/US099_COMB.pep:*/cgn2_6/ptodata/2/paa/US100_COMB.pep:*/cgn2_6/ptodata/2/paa/US101_COMB.pep:*/cgn2_6/ptodata/2/paa/US60_COMB.pep:*

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			Description		Seguence 9	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 2, Appli
SUMMARIES			ID		PCT-US99-31025-9	US-09-223-546-9	US-09-471-179-9	0-965-665-60-SD	US-09-796-753-12	NS-09-970-076-8	US-09-970-076-2
			DB		H	16	18	19	21	23	23
			ore Match Length DB II		333	333	333	333	333	333	368
	æ	Query	Match		100.0	100.0	100.0	100.0	100.0	100.0	95.4
			Score		1728	1728	1728	1728	1728	1728	1649
		Result	No.		-	7	٣	4	2	9	7

Sequence 94, Appl Sequence 621, App Sequence 61, App Sequence 187, App Sequence 232, App Sequence 6, Appl Sequence 125, App Sequence 125, App	9 62(30, 51, 6 30, e 51, e 132, e 132,	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	quence 59, A equence 59, quence 107, equence 2, Ap quence 2, Ap equence 52, equence 52,	(4 ,4 ,4
045-9 988-6 245-6 715-1 715-2 076-6 045-1	2 US-09-833-245-62 PCT-0899-31025-30 PCT-0899-31025-30 US-09-471-179-30 B US-09-471-179-51 PCT-0899-31025-13 DCT-0899-31025-13 US-09-918-715-19	3 US-09-918-715-30 PCT-US99-31025-50 B US-09-471-179-50 B US-09-471-179-50 B US-09-470-076-10 PCT-US99-31025-10 B US-09-370-076-10	PCT-10500-05226 US-1050-0516-745 PCT-10500-0516-745 US-109-516-745 US-109-516-745 US-09-796-745 US-09-796-745	6 US-60-318-905-2 6 US-60-322-468-6 6 US-60-322-733-6 6 US-60-322-793-1 6 US-60-324-050-2 6 US-60-324-050-2
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CIDS	100.0%; Score 1728; DB 1; Length 33:
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C. D NU	28;
Inc ANI 310:	17.
SULT 1 17-US9931025 Sequence 9, Application PC/TUS9931025 Sequence 9, Application PC/TUS931025 Sequence 9, Application: Sequence 9, Application: APPLICANT: Millennium Pharmaceticals, Inc. APPLICANT: Millennium Pharmaceticals, Inc. TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS TITLE OF INVENTION: ENCODING THEM FILE PEPRENCE: 7853-173-228 FURRENT APPLICATION NUMBER: PCT/US99/31025 CURRENT FILING DATE: 1999-12-3 EARLIER FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 135 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 333 TYPE: PRT ORCANISM: Homo sapiens TYPE: PRT	Score
ULT 1 1.0299-31025-9 equence 9 Application PC/TUS9931 ENERAL INFORMATION: APPLICANT: Millennium Pharmacetic. TITLE OF INVENTION: SECRETED PROT TITLE OF INVENTION: SECRETED PROT TITLE OF INVENTION: DADING THEM FILE REFERENCE: 7853-173-228 FURRENT FILING DATE: 1999-12-23 EARLIER FILING DATE: 1999-12-23 EARLIER FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 135 SOFTWARE: FastSEQ for Windows Ver. EQ ID NO EQ ID NO UNABLE OF SEQ ID NOS: 137 SOFTWARE: PRT ORGANISM: HOMO Sapiens	e 6
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Gaps 1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60 ö Indels 100.0%; Pred. No. 5.2e-168; Live 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 333; Conservative

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GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
                                                                                                    VRGNGFRHARNVDRYLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                              APPLICANT: Holtzman, Douglas
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: 9404/066012
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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Best Local Similarity 100.
Matches 333; Conservative
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US-09-223-546-9
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US-09-471-179-9
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US-09-223-546-9
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CURRENT APPLICATION NUMBER: 05/09/599,596
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
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100.0%; Pred. No. 5.2e-168;
iive 0; Mismatches 0;
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100.0%; Pred. No. 5.2e-168;
ive 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows version 3.0
SEQ ID NO 9
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEO ID NOS: 135
SOFTWARE: FastSEO for Windows Version 4.0
SEO ID NO 9
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Best Local Similarity 100.0
Matches 333; Conservative
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US-09-599-596-9
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US-09-471-179-9
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US-09-599-596-9
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Best Local Simi
Matches 333;
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TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-796-753-12
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EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
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CURRENT APPLICATION NUMBER: 09/09/796,753

CURRENT FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR PELING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-12-30

PRIOR FILING DATE: 1998-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-02-26

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-30

PRIOR PELING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/342,664

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/342,664

PRIOR PELING DATE: 1999-07-30

PRIOR PELICATION NUMBER: 09/474,072

PRIOR PELING DATE: 1999-07-30

PRIOR PELING DATE: 2000-03-01

PRIOR PELING DATE: 2000-03-03

PRIOR PELING DATE: 2000-
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5.2e-168;
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100.0%; Pred. No. 5.2e-168;
ive 0; Mismatches 0;
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Pred. No. 5.26
; Mismatches
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GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.97745
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CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 12
LENGTH: 333
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SEQ ID NO 8
LENGTH: 333
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Matches 333; Conservative
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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Pred. No. 8.9e-160;
0; Mismatches 0;
                                                                                       ; Gerricha Information:
Applicant: Human Genome Sciences, Inc.
Applicant: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPERENCE: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 201
SOFTWARE: PatentIn Ver: 2.0
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Sequence 621, Application PC/TUS0111988
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FCT
CURRENT APPLICATION NUMBER: PC1/201/11988
CURRENT APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/226, 931
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver: 2.1
                     RESULT 8
PCT-US00-30045-94
; Sequence 94, Application PC/TUS0030045
; GENERAL INFORMATION:
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100.0%; Pr
tive 0;
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Matches 318; Conservative
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PCT-US00-30045-94
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PCT-US01-11988-621
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TYPE: PRT
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SEQ ID NO 94
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100.0%; Pred. No. 7.7e-160;
Hive 0: Mismatches 0;
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Sequence 2 Application US/09970076
Sequence 2 Liver Sequence 2 Application US/09970076
Sequence 2 Sequence 2 Sequence 2 Applicant India, Applicant Bradley, Kenneth A. Applicant Collier, Robert J. Applicant Collier, Robert J. Applicant Collier, Robert J. Applicant Collier, Robert J. Applicant Sequence 360296.9748
FILE REFERENCE: 960296.9748
FILE REFERENCE: 960296.9748
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2001-10-03
SOFTWARE: PatentIn Ver. 2.1
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Matches 318; Conservat
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US-09-970-076-2
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                241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                                                                                                                                                                                                              Sequence 187, Application US/09918715
Seguence 187, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bret Vogelstein
APPLICANT: Reneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERENCE: 1107 (00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-01
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
SPIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastsEQ for Windows Version 3.0
LENGTH: 564
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100.0%; Pred. No. 1.5e-159;
11ve 0; Mismatches 0;
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US-09-918-715-232
; Sequence 232, Application US/09918715
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
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Matches 318; Conservative
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US-09-918-715-187
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                                                                 Score 1649; DB 1; I
Pred. No. 8.9e-160;
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100.0%; Pred. No. 8.9e-160;
iive 0; Mismatches 0;
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                                                                                                   0; Mismatches
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; ORGANISM: HOMO PCT-US01-11988-621
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APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: 05/022,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/281,850
PRIOR APPLICATION NUMBER: 60/281,850
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/281,850
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1.5e-159;
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; Sequence 6, Application US/09970076
; GRERAL INFORMATION:
    APPLICANT: Pandley, Kenneth A. APPLICANT: Collier, Renerth A. APPLICANT: Collier, Robert J. APPLICANT: Mogridge, Jeremy S. TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/09/970.076
; CURRENT FILING DATE: 2001-10-03
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; COGTWANTE: PATENTIN VOICE: 21
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100.0%; Pred. No. 1...
0; Mismatches
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GRGANISM: Homo sapiens
US-09-970-076-6
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US-09-918-715-232
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Best Local Similarity
Matches 318; Conserv
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LENGTH: 564
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US00-30045-125
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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VOTER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME,KEY: SITE
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Pred. No. 2.9e-159;
0; Mismatches 1;
95.4%; Score 1649; DB 23;
100.0%; Pred. No. 1.5e-159;
.ive 0; Mismatches 0;
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PCT-US00-30045-125
Sequence 125, Application PC/TUS0030045
Sequence 125, Application PC/TUS0030045
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT;
CURRENT PELICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-630
PRIOR FILING DATE: 2000-630
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         Query Match 95.4°
Best Local Similarity 100°.
Matches 318; Conservative
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LOCATION: (175)
OTHER INFORMATION: Xaa
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SOFTWARE: PatentIn Ve
SEQ ID NO 125
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Matches 317; Conserv
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE

1 LOCATION: (368)

2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-11988-620
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KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
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GEMERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT PAPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENTIN UNMER : 60/199, 384
PRIOR FILING DATE: 2000-04-25
SOFTWARE: PALENTIN UNMER : 2000-04-25
ILBUGTH: 403
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Best Local Similarity 99.77
Matches 317; Conservative
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Search completed: August 9, 2002, 10:44:32 Job time: 870 sec

Sequence 620, App Sequence 194, App Sequence 301, App

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Indels
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Pred. No. 3.1e-179;
Mismatches 0;
            PCT-USS1-11988-620

US-09-918-715-301

US-09-918-715-301

US-09-918-715-301

US-09-918-715-301

US-09-223-546-9

US-09-223-546-9

US-09-470-756-9

US-09-90-00-76-8

PCT-US99-31025-31

US-09-910-9132

PCT-US99-31025-51

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US-60-324-246-2
US-60-324-621-8
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GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.;
TITLE OF INVENTION: Anthreax Toxin Receptor;
FILE REFERENCE: 960296, 97745
CURRENT APPLICATION NUMBER: 08/09/970, 076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
SOFIWARE: PATENTING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
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ORGANISM: Homo sapiens
US-09-970-076-2
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Best Local Similarity
Matches 368; Conserv
US-09-970-076-2
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Sequence 187, App
Sequence 232, App
Sequence 6, Appli
Sequence 621, App
Sequence 621, App
                                                                                                                               (without alignments)
255.315 Million cell updates/sec
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-918-715-187
US-09-918-715-232
US-09-970-076-6
PCT-US00-11988-621
US-09-833-245-621
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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US-09-918-715-232
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US-09-970-076-6
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APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 00/225,599
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 187
LENGTH: 564
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100.0%; Pred. No. 5.4e-177;
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Best Local Similarity 100.
Matches 364; Conservative
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361 ESEENKIK 368
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                                                                                                                                                                                                         Sequence 232, Application US/09918715
Sequence 232, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Henreth Kinzler
APPLICANT: Kenneth Kinzler
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
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Pred. No. 5.4e-177;
0; Mismatches 0;
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Best Local Similarity 100.0%; P.
Matches 364; Conservative 0;
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Gaps

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HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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100.0%; Pred. No. 1e-176;
iive 0; Mismatches 0;
                                            98.7%; Score 1889; DB 1;
100.0%; Pred. No. 1e-176;
iive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TTLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
FROM THE OF SEQ ID NOS: 2267
SEQ ID NO 621
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Best Local Similarity
                                                              Similarity
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; ORGANISM: Homo
PCT-US01-11988-621
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 PCT-US00-30045-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATE: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 201
SOFTWARE: PATENTIN VET. 2.00
                        APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mgridge, Jeremy S.
TAPLICANT: Mgridge, Jeremy S.
TILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: 08/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
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PCT-USO0-30045-94
; Sequence 94, Application PC/TUS0030045
; GENERAL INFORMATION:
Sequence 6, Application US/09970076
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-970-076-6
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ORGANISM: Homo sapiens
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LENGTH: 403
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LENGTH: 564
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100.0%; Pred. No. 1e-176;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                          PARICAL INCOMENTATION: Albumin Fusion Proteins TITLE OF INVENTION: Albumin Fusion Proteins FILE REFERENCE: PF546FCT CURRENT APPLICATION UNMBER: US/09/833,245 CURRENT FILING DATE: 2001-04-12 PRIOR APPLICATION NUMBER: 60/256, 931 PRIOR FILING DATE: 2000-04-12 PRIOR FILING DATE: 2000-12-21 PRIOR FILING DATE: 2000-12-21 PRIOR FILING DATE: 2000-04-25 NUMBER: 6/199, 384 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 2267
                                                                                                                                                                                                                                       ; Sequence 621, Application US/09833245
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 363; Conservative
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US-09-833-245-621
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                                                                                                                                                                                                                                                                                                                                                                                                                        any of the naturally occurring L-amino acids
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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Sequence 125, Application PC/TUS0030045
Sequence 125, Application PC/TUS0030045
GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS/08PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 201
SSETURE OF SEC ID NOS: 201
SSETURE OF SEC ID NOS: 201
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Pred. No. 7.7e-175;
0; Mismatches 3;
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99.28;
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Best Local Similarity 99.2
Matches 360; Conservative
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NAME/KEY: SITE
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LOCATION: (320)
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NAME/KEY: SITE

COTHER INFORMATION: (175)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (120)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (331)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-11988-620
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                                APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/USO1/11988
CURRENT FILING DATE: 2001-01-12
PRIOR FILING DATE: 2000-04-12
PRIOR REPLICATION NUMBER: 60/226, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PILING DATE: 2000-12-21
PRIOR PRILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 620
Sequence 620, Application PC/TUS0111988 GENERAL INFORMATION:
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Matches 360; Conservative
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US-09-833-245-620
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LOCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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99.2%; Pred. No. 7.7e-175;
ive 0; Mismatches 3;
TITLE OF INVENTION SALDHAM FUSION FOLCEINS
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 620
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GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
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Matches 360; Conservative
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: X
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LOCATION: (368)
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US-09-918-715-194
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                          LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                                                                                                                                                                                                                                   9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ 68
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; Sequence 301, Application US/09918715
; GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Reneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-02
PRIOR PELICATION NUMBER: 60/222,599
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/228,850
PRIOR PELICATION NUMBER: 60/282,850
PRIOR PELICATION NUMBER: 2000-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                            Score 1793; DB 23;
Pred. No. 4.8e-167;
6; Mismatches 8;
    EXPRESSION
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESS FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FRAELSEQ for Windows Version 3.0
SSOFTWARE: FASTESQ for Windows Version 3.0
SSOFTWARE: 562
                                                                                                                                                                                                                                                                              93.7%;
96.1%;
                                                                                                                                                                                                                                                                                                            Conservative
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ORGANISM: Mus musculus
US-09-918-715-194
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Best Local Similarity
Matches 342; Conserv
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US-09-918-715-301
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                                                                                                                  EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
                                                                                                                                                                                               ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH 248
                                                                                                                                                                                                                                                                                                      249 ARNVDRVICSFKINDSVTLNEKPFSVEDIYILCPAPIIKEVGMKAALQVSMNDGLSFISS 308
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                           SVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEESEE 364
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Sequence 9, Application PC/TUS9931025
GENERAL INFORMATION:
TITLE OF INVENTION: BECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: BECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: BECRETED PROTEINS AND NUCLEIC ACIDS
FILE REPERBACE: 7853-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT FILING DATE: 1999-12-23
EARLIER RILING DATE: 1999-12-33
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FRALSEQ for Windows Version 4.0
SEQ ID NO 9.
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                              Indels
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100.0%; Pred. No. 3.5e-153;
iive 0; Mismatches 0;
Score 1793; DB 23;
Pred. No. 4.8e-167;
6; Mismatches 8;
      93.7%;
96.1%;
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Matches 318; Conservative
                                   Conservative
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; ORGANISM: Homo sapiens
PCT-US99-31025-9
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                        Similarity
                                      Matches 342;
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completed: August
ne: 867 sec
                 Query Match
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Job time: {
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MATAERRALGIGFOWLSLATLVLICAGOGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
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9 (26.09-47)-179-9
1 Sequence 9. Application US/09471179
2 Sequence 9. Application US/09471179
3 GENERAL INFORMATION:
1 APPLICANT: Holtzman, Douglas
2 TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
3 FILE REFERENCE: 7853-173
3 CURRENT APPLICATION NUMBER: US/09/471,179
5 CURRENT APPLICATION NUMBER: US/09/471,179
6 PRIOR APPLICATION NUMBER: 1999-12-23
7 NUMBER: OF SEQ ID NOS: 135
7 SEQ ID NOS: 135
7 SEQ ID NO 9
                                                                                                                                             Sequence 9, Application US/09223546
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Holtzman, Douglas
FILE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE OF INVENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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100.0%; Pred. No. 3.5e-153;
tive 0; Mismatches 0;
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Matches 318; Conservative
                                                   301 DGLSFISSSVIITTHCS
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo sapiens
US-09-223-546-9
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US-09-471-179-9
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                               Gaps
                                                                     1 MATAERRALGIGFQWLSLATLVLICAGGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
                                                                                                                                                           HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
      Length 333;
                               Indels
       Score 1649; DB 18;
Pred. No. 3.5e-153;
86.2%; Scool 100.0%; Pred. No. ...
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                     Best Local Similarity 100.
Matches 318; Conservative
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99, Appl 2, Appli 2, Appli 99, Appl

Searched:

Sequence:

Run on:

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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 99, Appl
Sequence 99, Appli
Sequence 99, Appli
Sequence 43, Appli
Sequence 43, Appli
Sequence 43, Appli
Sequence 43, Appli
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Sequence 46, Application US/08286889
Patent No. 5470953
GEMERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Gallatin, W. Mich
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS: 51
CORRESPONDENCE ADDRESS: 52
CORRESPONDENCE ADDRESS: 53
CORPESSE: Marshall, O'Toole, Gersteln, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STREET: 111nois
COMPUTER: Rebable FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURSIFICATION UNABER: US/08/286,889
FILING DATE:
CLASSIFICATION 473
APPLICATION NUMBER: US 08/173,497
FILING DATE: 33-DEC-193
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 27866/32168
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
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28.9%; Pred. No. 6.8e-06;
tive 31; Mismatches 69
                    US-08-485-618-2
US-08-485-618-9
US-08-485-618-99
US-08-605-672-2
US-08-605-672-99
US-08-482-293A-2
US-08-943-363-2
US-08-943-363-2
US-09-193-043-99
US-09-193-043-99
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PCT-US96-01314-43
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US-08-286-889-3
US-08-485-618-3
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INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
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Matches 50; Conservative
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  Query Match
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117.080 Million cell updates/sec
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1 MSFIVFSTRGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT 218
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Sequence 53,
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Sequence 46,
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-36-52-46
US-08-36-55-46
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US-08-413-61-46
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US-08-613-618-37
US-08-193-043-53
US-08-365-237
US-08-365-337
US-08-365-337
US-08-365-337
US-08-365-55
US-08-485-618-55
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Result

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Gaps

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260 DGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVFK 316
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260 DGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVFK 316
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                                                                                                                                      Indels
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233 South Wacker Drive, 6300 Sear Tower
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MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN NATA:
APPLICATION NUMBER: US/08/362,652
PRIOR APPLICATION NUMBER: US/08/362,652
PRIOR APPLICATION NUMBER: US/08/362,652
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTONEY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTONEY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTONEY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 08/286,889
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ilarity 28.9%; Pred. No. 6.8e-06;
Conservative 31; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
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APPLICANT: Van der Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monicante Vieren, Monican
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REPERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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COUNTRY: United States
ZIP: 60606-6402
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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Best Local Similarity
Matches 50; Conserv
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STREET: 23
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US-08-362-652-46
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                                                        205 TEFKSSLSPOSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
                                                                                                                                                                         71 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application US/08485618
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: AD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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28.9%; Pred. No. 6.8e-06;
tive 31; Mismatches 69
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CLASSIFFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US
REPLICATION NUMBER: US
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
RAPLICATION NUMBER: US
ATORNEY/AGENT INFORWATION:
NAME: Williams JT., JOSEPH ATORNEY/AGENT INFORWATION:
REPERENCE/DOCKET UNMBER: 38,659
REFERENCE/DOCKET UNMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 60606-6402
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Best Local Similarity
Matches 50; Conserva
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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US-08-485-618-46
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205 TEFKSSLSPQSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
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Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
       APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                                                                                                                                                                                                                                  ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
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Best Local Similarity 28.9%; Pred. No. 6.8e-06;
Matches 50; Conservative 31; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-194
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                        2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%; Score 128.5; DB 2; 28.9%; Pred. No. 6.8e-06; tive 31; Mismatches 69;
                              Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human
UNMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGGNT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
BREDERWICH AND NUMBER: 38,659
BREDERWICH AND NUMBER: 38,659
BREDERWICH AND NUMBER: 38,659
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APPLICATION NUMBER: US/08/605,672
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GENERAL INFORMATION: GENERAL SPECIAL SP
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TELECHONE: 312-474-6300
TELEFRONE: 312-474-6448
TELEFX: 25-3856
INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 1155 amino acids
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Best Local Similarity
Matches 50; Conserv
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US-08-605-672-46
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71 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
TITLE OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
CORRESPONDENCE MATSHALL, O'TOOLE, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.9%; Pred. No. 6.8e-06;
Matches 50; Conservative 31; Mismatches 69; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | : | | : | | : | | | 364
317 VGN-FVALRSIQRQIOEK----IFAIBGTESRSSSFRHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: 111inois
STATE: 111inois
STATE: 111inois
SCONTRY: United States
ZIP: 60606-6402
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
COMPUTER: PSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: APELICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMONICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-6448
TELERAX: 25-3856
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US APPLICATION NUMBER: US RELING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: STILNG DATE: 21-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
BARLIER FILING DATE: 1994-12-21
BARLIER APPLICATION NUMBER: 08/943,363
BARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
LENGTH: 1155
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US-08-485-618-53
Second 53, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 TEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1155;
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                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 128.5; DB 2; 28.9%; Pred. No. 6.8e-06; tive 31; Mismatches 69;
                                        : 233 South Wacker Drive, 6300 Sear Tower Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TILE OF INVENTION: No. 6551395el Human 2
TILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER FILING DATE: 1998-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/362,652
                                                                                                                                                                                                                                                                                                                                                                 CLASSLETCRILON: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-MG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY,AGENT INFORMATION:
NAME: Williams Jr. JOSeph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 37866/32684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/09193043
Patent No. 6251395
                                                                                                                                              ZIP: 60606-6402
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: Floppy disk
CMEDIUR: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELER. 312-4.
TELERS 25.3856
INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
"VPE: amino acids
'inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.4%
Best Local Similarity 28.9%
Matches 50; Conservative
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                                                                                                                   COUNTRY: United States ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
                                                                           CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-09-193-043-46
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                    12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQCYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 Integrin Alpha Subunit
                                                                                                                                                                                              23;
                                                                                                                                               11.4%; Score 128.5; DB 1; Length 1161; 28.9%; Pred. No. 6.9e-06; tive 31; Mismatches 69; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                          122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Marshall, O'Toole, Gerstein, Murray & Borun
:: 233 South Wacker Drive, 6300 Sear Tower
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: 111inois
COUNTRY: United States
ZIP: 6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BY PC compatible
COMPUTER: BY PC compatible
COMPUTER: BY PC compatible
COMPUTER: BY PC compatible
COMPUTER: BY PC compatible
COMPUTER: BY PC compatible
SOFTAME: PATENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: MAISHALL, O'Toole, Gerstein, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMONICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
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1161 amino acids
                                                                                                                                                                        Best Local Similarity 28.9
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                    ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-618-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-362-652-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-362-652-53
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  LENGTH:
                                                                                                                                                 Query Match
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                         23; Gaps
                                                                       12 TLMKLTEDREQIRQCLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 351/21.
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
ATTLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
TITLE OF INVENTION: 103
                                                                                                                                                                                                                                                                      122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: 111inois STATE: 111inois COUNTRY: United States IP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                         Indels
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CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.4%; Score 128.5; DB 2 Best Local Similarity 28.9%; Pred. No. 6.9e-06; Matches 50; Conservative 31; Mismatches 69
Best Local Similarity 28.9%; Pred. No. 6.9e-06;
Matches 50; Conservative 31; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Application US/08605672 Patent No. 5817515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 312-474-6300
312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
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Query Match

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122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD
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CLASSIFICATION: 530
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
FILING DATE: 12-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
FILING DATE: 10-DEC-1994
                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 27866 TELECOMMUNICATION INFORMATION: TELECHHONE: 312-474-6300
                                                                                                                    sequence 53, Application US/08943363 Patent No. 5837478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-474-0448
TELEX: 25-3856
INPERMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACIERISTICS:
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Best Local Similarity
Matches 50; Conserva'
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                                                                                                                                                                                                                                                                                                           Illinois
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US-08-943-363-53
                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illino
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                                                                                                RESULT 12
US-08-943-363-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Gaps
                                                          260 DGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVFK 316
     205 TEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
                                    71 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
                                                                                                                                                                                        Length 1161;
                                                                                                      122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 128.5; DB 2
11arity 28.9%; Pred. No. 6.9e-06;
Conservative 31; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGGNT INFORMATION:
NAME: Williams JI , Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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205 TEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                  APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADRESSE:
ADRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1161;
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
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ilarity 28.9%; Pred. No. 6.9e-06;
Conservative 31; Mismatches 69
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FILING DATE:
CLASSIPICATION: 435
PIONE APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 37, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 233 South Wacker
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
FILING DATE: 23-DEC-1993
                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.77
Matches 52; Conservative
                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-889-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
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ZIP: 60606-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.4%; Score 128.5; DB 4
28.9%; Pred. No. 6.9e-06;
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                                                                                                                         APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Wichael W.
TITLE OF INVENTION: No. 62513551 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/13,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SECTIANRE: PATENTING VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                            Sequence 53, Application US/09193043
Patent No. 6251395
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US-09-193-043-53
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Best Local Similarity
Matches 50; Conserva
                                                                                                             GENERAL INFORMATION:
                                          US-09-193-043-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 RQCYRTA-SVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLAR 111
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 122; DB 1; Length 1151; 27.7%; Pred. No. 3.9e-05; tive 32; Mismatches 76; Indels 28
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233 South Wacker Drive, 6300 Sear Tower
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUFRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/485,618
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
TELEFRAX: 312-474-6448
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Best Local Similarity 27.7%; Pred. No. 3.9e-05;
Matches 52; Conservative 32; Mismatches 76; Indels 26
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CARRACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: protein
US-08-485-618-37
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Search completed: August 9, 2002, 10:33:12 Job time: 191 sec

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09f49 arabidopsis

09f2v10 arabidopsis

091311 salmonella

0912f5 caenorhabdi

04285 arabidopsis

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069681 bomo sapien

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06731 bacillus su

074080 pyrococcus

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O43981 eimeria ten
O9aiu3 ehrlichia p
        019319 caenorhabdi
096ft5 homo sapien
09p218 homo sapien
09bqu7 homo sapien
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005707 homo sapien
097566 canis famil
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096191 homo sapien
P89140 pseudorabie
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butaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostoml;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last sequence update)
Last annotation update)
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096nc7 homo sapien
096ec6 homo sapien
09bpq8 halocynthia
09gye7 rattus norv
043853 homo sapien
070350 mus musculu
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09ugc3 homo sapien

09ji30 rattus norv

09ji11 clostridium

09us03 schizosacch

096hx6 homo sapien

063870 mus musculu
                                                                                        9, 2002, 10:46:26 ; Search time 102.68 Seconds
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367.286 Million cell updates/sec
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1 MSFIVFSTRGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                                         NIONING R. Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., NIONING K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kamihara K., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Katsuta N., Sato H., Wakamutsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sato H., Wishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakwa K., Yamashita H., Karehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human CDNA sequencing project.";
Suzuki Led (OCT-2001) to the EMBL/Genbank/DDBJ databases.
Suzuki AKOS5636; Babl/Ost.;
SEQUENCE 245 AA; 26111 MW; BIAEGEBOAZEBEEGG CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                     01-DEC-2001 (TEMBLE): 19, Last sequence update)
01-DEC-2001 (TEMBLE): 19, Last annotation update)
CDNA FL31074 FIS, CLONE HSYRA2001476.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.7%; Score 506; DB 4; Length 245; 53.4%; Pred. No. 1.1e-38; tive 37; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-BREAST, AND MAMMARY ADENOCARCINOMA;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC012475; AAH12475.1; -.
NON_TER 1
SEQUENCE 97 AA; 10453 MW; 14F475F0B170E71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096EC6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
Homo sapiens (Human).
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                                                                                                                                     245 AA
                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequent-DEC-2001 (TrEMBLrel. 19, Last and
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Best Local Similarity 53.49
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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181 TVNETYTTS 189
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
260 KINDSVTLNE
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Q96EC6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- ASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 KLTEDREQIRQGLEELQXVLPG------GDTYMHEGFERASEQIYYENRQG 59
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                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyazawa S., Azumi K., Nonaka M.;
Miyazawa S., Azumi K., Nonaka M.;
"Cloning and charaction of integrin alpha subunits from the
"Cloning and charaction of integrin.";
Solitary ascidian, Halozythia roretzi.";
J. Immunol. 166:1710-1715(2001).
EMBL, ABO84561; BAB21479.1; -..
HSSP, 11215; 1A8X.
Interpro; IPR000413; Integrin_alpha.
Interpro; IPR000535; wWRA.
Pfam; PF001839; FG-GAP; 5.
Pfam; PF00182; vwa: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
INTEGRIN ALPHA HR1.
WW; 0D9108D2B05CFFAE CRC64;
                                   2; Indels
                                                                                                                                                                                                                                                                                                                                    Halocynthia roretzi (Sea squirt).
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
Length
                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Query Match
Best Local Similarity 87.9%; Pred. No. 1.6e-06;
Matches 29; Conservative 2; Mismatches 2
                                                                                                                                                                                                           PRT; 1332 AA.
                                                                         158 FQVVVRGNGFRHARNVDRVLCSFKINDSVTLSK 190
                                                                                               TISSUE-HEMOCYTE;
MEDLINE-21103187; PubMed=11160215;
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                                                                                                                                                                                                             PRELIMINARY;
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1332
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31 133
1332 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7729;
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93 GAIVYCVGVKD-FN----ETQLARIADSK--DHVFPVNDGFQALQGIIHSILKKSCIEIL 145
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                         37 GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSE--REANRSRDL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98003048; PubMed=9344363;
Messel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.;
Type XII collagen contributes to diversities in human corneal and
limbal extracellular matrices., Invest Ophthalmol. Vis. Sci. 38:2408-2422(1997).
EMBL: 068139; AACO1506.1; ...
Interpro; IPR003051; FN_III.
Interpro; IPR003055; WRA.
Pfam; PF00041; fn3; 3.
Pfam; PF00042; vwa: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                   Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                             102440 MW; E96CC51E350DD5AC CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TYPE XII COLLAGEN (FRAGMENT).
                                                                                                                                                                                                                              55;
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                                                                                                                                                                                                   ch 9.6%; Score 109; DB 6; 1. Similarity 29.0%; Pred. No. 0.24; 42; Conservative 28; Mismatches 55
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26.0%; Pred. No. 0.15;
tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 AA.
HSSP; P11215; 1A8X.
InterPro: IPR000413; Integrin_alpha.
InterPro: IPR00023; vwFA.
Pfam; PF001839; FG-GAP; 4.
Pfam; PF00185; vwa; 1.
PR.NTS; PR00185; INTEGRINA.
PR.NTS; PR00453; VWFADOMAIN.
SMATT; SM00191; Int_abha; 4.
SMART; SM00137; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                  146 AAEPSTICAGESFQVVVRGNGFRHA 170
                                                                                                                                                                                                                                                                                                                                                                                      201 AIEGTQTGSTSSFECEMSQEGFSAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 3.
SMART; SM00327; VWA; 1.
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Best Local Similarity
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                                                                                                                                                             920 AA;
                                                                                                                                                                                                     Query Match
Best Local Similarity
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NON_TER
NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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043853
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                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 I----ADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 LNTIGSAPPODHVFKVGN-FAALRSIQRQLQEK----IFAIEGTQSRSSSSFQHEMSQEG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 RQGYRTA-SVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLAR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 NGSRKSAKKILLVITDGQKYRDPLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFIVFSTRGTTLMKLTE----DREQIRGCLEELQKVLPGGDTYMHEGFERASEQIYYEN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 122; DB 11; Length 1161; 27.7%; Pred. No. 0.021; Live 32; Mismatches 76; Indels 28
                                                                                                                                                                        O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                      2258491A984A705E CRC64;
                                                                                                                                                                                                SEQUENCE FROM N.A.
Lee J.-K., Schook L.B., Rutherford M.S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL. U40072; ABB1686911; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                       Last sequence update)
Last annotation update)
PRT; 1161 AA
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                            Created)
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PROSITE; PS50234; VWFA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     1161 AA; 126600 MW;
                                                                                                                                                                                                                                                                            Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                          Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SW00191; Int_alpha; 4.
SWART; SM00327; VWA; 1.
                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.8%
Best Local Similarity 27.7%
Matches 52; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY;
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Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                ALPHA D INTEGRIN.
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                                                                                                                                         FQALQGIIHSILKKSCIEI---LAA-----EPSTICAGESFQVVVRGNGFRHARNVDR 175
                                                                                                                                                                                   303 FDAFQRISFELTQSICLRIEQELAAIKKKAYVPPKDLSFSEVTSYGFKTNWSPAGENVFS 362
                                                                                  248 LITDGK-SSDAF---RDPAIKLRNSDVEIFAVGVKDAVDSELEAIASPPAETHVFTVED- 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                         68 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDG 125
Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBankIV S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
TRYPSIN FAMILY.
EMBL; ARC094065. AAC04162.1; -.
EMBL; ARC049850; AAC04162.1; -.
EMBL; BC011086; AAH11086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.
                                                                                                                                                                                                                             176 VLCSFKI---NDSVTLSKSLQSP------WVSSTSGFKEGNSHP 210
                                                                                                                                                                                                                                                      363 YHITYKEAAGDDEVIVVEPASSISVVLNSLKPETLYLVNVTAEYEDGFSIP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1999 (TremBirel. 11, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91C896A3EDC7D448 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    760 AA.
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MGD: MGI:88226; G2.

InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR00124; Trypsin.
InterPro: IPR00125; vWFA.
Pfam: PF00084; sushi. 2.
Pfam: PF00089; trypsin. 2.
Pfam: PF00089; trypsin. 2.
Pfam: PF00089; trypsin. 2.
PRINTS: PR00722; CHYMOTRYPSIN.
PRINTS: PR00453; VWFADOMAIN.
SWART; SM00032; CPT. 2.
SWART; SM00032; CPT. 2.
SWART; SM00032; CPT. 2.
PROSITE; PS00134; TRYPSIN.JES; UNKNOW PROSITE; PS00134; TRYPSIN.JES; UNKNOW PROSITE; PS00135; TRYPSIN.JES; TRYPS
                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequ
01-DEC-2001 (TrEMBLrel. 19. Last semi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 291-760 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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MEDLINE-93149203; PubMed-8426611;

A pasamontes L.E., Hug D., Huembelin M., Weber G.;

Pasamontes L.E., Hug D., Huembelin M., Weber G.;

Pasamontes of a major Eimeria maxima antigen homologous to the Eimeria maxima in tenella microneme protein Etplo00 ";

Mol. Bicchem. Parasitol. 57:171-174(1993).

R EMBL; M99058; AAA29076.1; -..

R EMBL; M99058; AAA29076.1; -..

R FATHY: PRO00099; twp.1; 6.

R FATHY: SM00209; twp.1; 6.

R SMART; SM00209; TSP1; 6.

R SMART; SM00209; TSP1; 6.

R PROSITE: PS50234; VWRP1; 5.

R PROSITE: PS50234; VWRP1; 5.

R PROSITE: PS50234; VWRP1; 5.
                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 GYR--TASVIIALTDGELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 GGRDNAPKMILVWTDGA-----SSRRSQTLSAABKLRNRGVIIVVLGVGTGVNSAEC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 VGLVTFGTSAVTRWDLSDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQ 58
                                                                                                                                                                                                                                                          ---VYCVGV-----KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEIL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 ARIA--DSKDHV-FP--VNDGFQALQGIIHSILKKSCIEI----LAAEPSTI--CAGE 156
                                                                                                                                                                                                     354 YSWMQSQMDRLGMETRHTILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDD 411
                                                                                                                                                                                                                                                                                               412 YLDIYAIGVGKLDVDWKELNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVSKL--- 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 VALITERASQPKTIMSILSERSQ-----DVTEVITSLDSASYKDHENATGTNTYEVLIRV 353
                                                                                                                                                                      ------ NRQGYRTAS----- VIIALTDGELHEDLFFYSEREANRSRDLGAI----- 95
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriidae;
                                                                                   1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE----
                                                                                                                                                                                                                                                                                                                                                                           466 ---TDTICG------VGNMSANASDQERTPWQVTFKPKSKETCQGSLISDQWV 509
                                                                                                                                                                                                                                                                                                                                                146 AAEPSTICAGESFQVVVRGNGFRHARNVDRV--LCSFKINDSVTLSKSLQS-PWV 197
                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 724;
Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR ANTIGEN HOMOLOGOUS SEQUENCE (EMP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.3%; Score 105.5; DB 5;
27.0%; Pred. No. 0.37;
Live 28; Mismatches 71;
      DB 11;
                                              77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŕ
    9.4%; Score 106.5; DE 24.3%; Pred. No. 0.32; Live 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.09
Matches 48; Conservative
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
             Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eimeria.
NCBI_TaxID=5804;
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Q63001
ID Q6
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GTQTGSTSSFEHEMSQEGFSAA 358
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Best Local Similarity 28.2%
Matches 40; Conservative
PROSITE; PS50234; VWFA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                        999
                                                           660 AA;
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                   Collagen.
NON_TER
SEQUENCE
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Q9JI30
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                                                                                                                                                                                                            STRAIN-WISTAR KYOTO;

C STRAIN-WISTAR KYOTO;

A Nablika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,

A Nablika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,

A Ulier C., Masuda J., Yamori Y., Nara Y.;

Comparative mapping of a hypertension-related region on rat

T "Comparative mapping of a hypertension-related region on rat

C Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U59801; AAB03226.1; -.

R HSSP; P11215; 1A8X.

R HSSP; P11215; 1A8X.

R THERPOOLS YOUR A.

P Fam.; PF00092; vwa: 1.

PRINTS; PR00453; vWFADOMAIN.

SMART; SM00327; vWa: 1.

R PRINTS; PR00453; vWFADOMAIN.

SMART; SM0327; vWa: 1.

R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R PNOW R 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 VYCVGVKD-FNETQLARIAD-----SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDTYMHEGFERASEQIYYE-NRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.2%; Score 104; DB 11; Length 205; Best Local Similarity 28.2%; Pred. No. 0.094; Matches 40; Conservative 24; Mismatches 64; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith M.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AL080250; CAB65984.1; ..
HSSP: P11215; 1BHQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA; 22922 MW; C8C2D9395008DA36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ234P15.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT)
              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTECRIN ALPHA-W (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003961; FN_III. InterPro; IPR002035; vWFA.
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Pfam; PF00092; vwa; 2.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM00327; VWA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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01-07-2000 (TrEMBLrel. 15, Last sequence update)
01-05C-2001 (TrEMBLrel. 15, Last sequence update)
INTEGRIN BETA 2 ALPHA SUBUNIT.
Rattus norveques (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 VYCVGVKD-FNETQLARIAD-----SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAE 148
                                                                                                                                                                                                                                                                    522 TLKKFTKVEDII-----EAINTFPYRGGSTNTGKAMTYVREKIFVPSK-GSRSNVPKVMI 575
                                                                                                                                                                                                                                                                                                                                68 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                            12 TLMKLTEDREQIRQCLEELQKVLP -- GGDTYMHEGFERASEQIYYENRQGYRT -- ASVII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Gaps
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                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.1%; Score 103; DB 11; Length 1151;
28.2%; Pred. No. 1.2;
Live 24; Mismatches 64; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fathallah D.M. Str., Zerria K. Jr.;

Rathallah D.M. Str., Zerria K. Jr.;

"Cloning of the rat CDllb CDNA sequence.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF26859; AAR81280.11 - ...

R HSPS; Pil215; 1A8X.

InterPro; IPR000413; Integrin_alpha.

R InterPro; IPR000435; VWFA.

R Pfam; PF001839; FG-GAP; 5.

R Pfam; PF001839; FG-GAP; 5.

R Pfam; PF000925; VWex J.

R PRINTS; PR01185; Integrin_A; 1.

R PRINTS; PR01095; Integrin_A; 1.

R SMART; SM00191; Int.alpha; 5.

R SMART; SM00191; Int.alpha; 5.

R SMART; SW00192; VWA: 1.

R PR0SITE; PS00242; INTEGRIN_ALPHA; 1.
                                                                                 Query Match 9.1%; Score 103; DB 4; Length 660; Best Local Similarity 31.0%; Pred. No. 0.55; Matches 45; Conservative 22; Mismatches 58; Indels
72523 MW; 3E3A10A285ECAA51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 FQALQGIIHSILKKSCIEI---LAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631 FDAFORISFELTOSICLRIEGELAA 655
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Query Match
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                                                                                                                                                                                         SEQUENCE FROM N.A.

SCHAIN-ATCC 824 / NEW B-1787;

STATIN-ATCC 824 / SUBMED-11466286;

MEDLINE-21359325; PubMed-11466286;

A MEDLINE-21359325; PubMed-11466286;

A Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

A Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

A Tatusov R.L., Sabathe E.V., Smith D.R.;

A Bennett G.N., Koonin E.V., Smith D.R.;

T Genome sequence and comparative analysis of the solvent-producing

T Dacterium Clostridium acetobutyjicum.";

E BAIL, AERON561; AAX78453.1;

B FAIL, AERON5561; AAX78453.1;

B FAIL, REWILS, PRO01035; VWFA.

NR FAIL PRO01021; HSP70.1.

R PRINTS; PRO0301; HEATSHOCK70.

R PRANTS; PRO0301; HEATSHOCK70.

R PROSITE; PS000329; HSP70.1;

NR PROSITE; PS000329; HSP70.2; 1.

R PROSITE; PS000329; HSP70.2; 1.

R PROSITE; PS000329; HSP70.2; 1.

R PROSITE; PS000329; HSP70.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTASVIIALTDGELHEDLFFYSER----EANRSRDLGAIVYCVGVKDFNETQLARIADSK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           605 GDCFVVV-LIDGQ------WYGKKDIMAEVNKCKEYEIEIAAIGFGNAKKDFLDKIAICE 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S50 LALIGFADKVKTLINLTEDREEFFRAIDGLKKADVGTST-MSEPFSEA----YNILKDAY 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                      01-001-2001 (TrEMBLrel. 18, Created)
01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-007-2001 (TrEMBLrel. 19, Last annotation update)
01-05C-2001 (TrEMBLrel. 19, Last annotation update)
DNAK PROTEIN (HEAT SHOCK PROTEIN), C-TERMINAL REGION HAS VWA TYPE
                                                                                                                      Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.8%; Score 99; DB 16; Length 698; llarity 27.0%; Pred. No. 1.4; Conservative 28; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPAC664.10.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                               698 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    817
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                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9US03;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINESIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=1488;
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EN 659
                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat shock;
SEQUENCE 6
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                                                                                                           A DOMAIN.
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Q9US03
                                 097LT1
097LT1;
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           RESULT 13
                       097LT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ELHEDLFFYSERBANRSRDLGAIVYCVG--VKDFNETQLARIADSKDHVFPVNDGFQA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 DGELHEDLFFYSE------REANRSRDLGAIVYCVGVKDFNETQLARIADSKDH--V 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F----PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFR-HARNV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 SAIQPLQEENNSLKQQIEQLQREL-ASETVVKENLKSSLDQ-QSANVQKLESTNRALEST 417
                                                                                                                                                                                                                                                                                                                                                                            31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 11 TTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 IDEIRDLLYIGKDRKNPREDYLDVYVFGVGPLVNQVNINALASKKDNEQHVFKVKD-MEN
Cadieu E., Lelaure V., Galibert F., McDougall R.C., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                    DB 3; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 95; DB 4; Length 764; 20.3%; Pred. No. 3.7; tive 32; Mismatches 69; Indels
                                       Delicit books (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI3623; CAB65811.1; -.
EMBL; ALI3623; CAB65811.1; -.
EMBL; ALI3623; Kines.
Interpro; IPR001752; Kinesin.
R PARNYS; PR00380; KINESINHEAVY.
R PRINTS; PR00380; KINESINHEAVY.
R PRINTS; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
R PROSITE; PS00411; KINESIN_MOTOR_DOMAIN2; 1.
R PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
R ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 817 AA; 91043 MM; 804677851AF1A52D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 RQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDG--
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC007990; AAH07990.1; -.
SEQUENCE 764 AA; 85563 MW; 7574383E5FF7CC95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                88;
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.1%; Pred. No. 2.9;
Matches 51; Conservative 33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 DRVLCSFKINDSV--TLSKSLQS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=COLON ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 42; Conserv
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189 SKSLQSPWVSSTSGFKEGNSH-PCLPA 214
: | | : | | : | | : | 490 --YHKQPWQAKISVIRPSKGHESCMGA 514 o S

Search completed: August 9, 2002, 10:46:28 Job time: 851 sec

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9, 2002, 10:47:07; search time 31.3 Seconds (without alignments) 269.676 Million cell updates/sec
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homo sapien
oryctolagus
homo sapien
gallus gall
mus musculu
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mus musculu
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mus musculu
homo sapien
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mus musculu
homo sapien
homo sapien
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homo sapien
caenorhabdi
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arabidopsis
arabidopsis
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homo sapien
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helicobacte
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                              1131
1 MSFIVFSTRGTTLMKLTEDR......STSGFKEGNSHPCLPARPHT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090cz52
0958335
058335
091334
0915255
091145
091145
0901145
000971
028902
000751
0042401
0042401
006238
000338
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067016
008746
P04186
P14677
Q92599
Q06967
Q06967
P18785
P18785
P18785
P18785
 4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                   105224 seqs, 38719550 residues
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GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATR_MOUSE
CMG2_HUWAN
CA1C_CHICK
CA1C_CHICK
ITAM_MOUSE
ITAM_MOUSE
CA1C_MOUSE
CA1C_HUWAN
CA1C_HUWAN
CA1C_CHICK
CAAR_HUWAN
CAAR_HUWAN
CAAR_CHICK
CAAR_HUWAN
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YNX3_CAEEL
Y849_AQUAET
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MTN2_HUMAN
CA17_HUMAN
PHOO_SALTY
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PBPX_STRPN
DPO1_HELPJ
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1433_ORYSA
1437_ARATH
PRH_ARATH
CA36_CHICK
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Maximum Match 100%
Listing first 45 summaries
                                                          using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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N-LINKED (GLCNAC. ..) (POTENTIAL).
EDDD -> NKIK (IN ISOPORM 2).
MISSING (IN ISOPORM 2).
NEKPESVEDTYLLCPAPILKEVGMKAALQV.-> SKSLQSP
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DGSILAIALLILFIL -> LHKIASGPTTAACME (IN
                                                                                                  Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                        1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                          ;
0
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Antrax toxin receptor precursor (Tumor endothelial marker 8).
ATR OR TEM8.
                                                                                                                                                                                                                                                                                       Score 966; DB 1; Length 564;
Pred. No. 4e-76;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDIINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.)
                                                                                                                                                          ASP/GLU-RICH (HIGHLY ACIDIC). PRO-RICH.
                                                                                                                FOIENTIAL.
ANTRAX TOXIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                     ISOFORM 4).
MISSING (IN ISOFORM 4).
B118A00AD5DF2233 CRC64;
                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562
                                                                                                                                                                                                                                                    ISOFORM 4)
                                          EMBL; AK025429; BAB15128.1; ALT_INIT.
EMBL; AK001463; BAA91707.1; ALT_FRAME.
EMBL; BC012074; AAH12074.1; -
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                                                                                                                                                                                                                                                                    62789 MW;
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98.9%;
                                     EMBL; AF279145; AAK52094.1; -
                                                                            InterPro; IPR002035; vWFA.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.9
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                     Receptor; Transmembrane; SIGNAL 1 32
                                                                                                                                             564
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260 KINDSVTLNE 269
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564 AA;
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ID ATR_MOUSE
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SEQUENCE
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                                                                                                                                                                                                 RA Kavai J. Shinagawa A. Shibata K., Yoshino M., Itoh M., Ishii Y.,
Ravai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Satto T., Okazaki Y., Golobori T., Bono H., Rasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsud H.A., Ashburner M., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarets P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Nayashibak'saki V.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
GRCINFTRVKNSQPAKYPLNNTYHPSSPPPARIYTPPPPAP
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RPSV -> RFRGWRLTICLGSKHVHFGRHDKGPETPLLKQA
WMFSSFLERAFQ (IN ISOFORM 2).
6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK013005; BAB28591.1; ALT_INIT.
MGD; MGI:1919432; Atr.
Interpro; IPR002035; VWFA.
PROSITE; PS50234; VWFA; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing
St Croix B.,; tumor endothelial markers are conserved in mice and tumor endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
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ANTRAX TOXIN RECEPTOR
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Pred. No. 1.3e-75;
                                                                                                                                        (ISOFORM 2).
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EMBL; AK013005; BAB28591.1; ALT_INIT.
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                                                                                                                                     SEQUENCE OF 88-562 FROM N.A. (ISOFK
STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-21085660; Pubmed=11217851;
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                                                                                     Cancer Res. 61:6649-6655(2001).
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'Cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercations and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21539596; PubMed-11683410; MEDLINE-21539596; PubMed-11683410; Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Tolfferential S.E., Tolfferential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling."; J. Cell Sci. 114:2755-2773(2001).

1: SUBGNITT: Seems to bind to collagen type IV and laminin.

1: SUBCELLULAR LOCATION: Type I membrane protein (Probable).

1: SIMILARITY: BELONGS TO THE ATR FAMILY.

1: SIMILARITY: CONTAINS I WWFA DOMAIN.
                                                                                                                                                          RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                               Gaps
                                MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Edkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarihini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAPILLARY MORPHOGENESIS PROTEIN-2. EXTRACELLULAR (POTENTIAL).
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   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Swiss Institute of Bioinformatics and the
 Indels
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0F9B2D6688EAB17A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Capillary morphogenesis protein-2 precursor (CMG-2).
 ij
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                           386 AA
 Mismatches
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 Conservative
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386 AA;
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Matches 187;
                                                                                                                                                                                                                                                                                                                                          CMG2_HUMAN
P58335;
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SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE-90257-236; Pubmed-8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH VCAM1.
MEDLINE-99059842; PubMed-9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 1-235 FROM N.A.
MEDLINE-20187620; PubMed-10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
Structural and functional characterization of the leukocyte integrin
gene CD11d. Essential role of Sp1 and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                    RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                    197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unton D.E., Gallatin W.M.;
novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
LSFIVFSSQATIILPLTGDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQI--OKAGGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-9937002: PubMed-10438935;
Wan der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
"The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding integrine between I domain and VCAM-1.";
J. Immunol. 163:1984-1990(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: INTEGRIN ALPHA-D/BETA-2 IS A RECEPTOR FOR ICAM3 AND VCAM1. MAY DATA A ROLE IN THE ATHEROSCIENTIC PROCESS SUCH AS CLEARING LIPOPROTEINS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOODBORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATES WITH BETA-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL
                                                                                                                                                                                                                                                                                                                       D) (CD11d) (ADB2).
                                                     Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    St John
                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                                                               013349; Q15575; Q15576;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MRA-2002 (Rel. 41, Last annotation update)
Integrin alpha-D precursor (Leukointegrin alpha
                                                                                                                                                                                                                                1162 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta 2-integrin alpha subunit.";
Gene 171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunity 3:683-690(1995).
                                                                                                         PVNDGFQALQGIIHS 135
                                                                                                                               STANDARD;
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1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60

33.0%; Score 373; DB 1; Length 386; 57.0%; Pred. No. 4.7e-25; ive 26; Mismatches 30; Indels

Conservative

77;

Matches

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Best Local Similarity

Query Match

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2846-2873
CARBOHYD
CONFLICT
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 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
INTEGRIN ALPHA-D.
EXTRACELLULAR (POTENTIAL).
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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FG-GAP 2.
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PROSITE; PS50234; VWFA; 1.
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Interpro; IPR002035; vWFA.
                                                                                                                                                                                                                                       EMBL; U37028; AAB38547.1; --
EMBL; U40274; AAB60634.1; --
EMBL; U40275; AAB60635.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40279; AAB60638.1; --
EMBL; U40278; AAB60638.1; --
EMBL; AF187881; AAF62875.1; --
HSSP; P11215; 1A8X.
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00357; integrin_A; 1. Pfam; PF00092; vwa; 1. PRINTS; PR01185; INTEGRINA. PRINTS; PR00453; VWFADOMAIN. SMART; SM0191; Int_alpha; 4. SMART; SM01927; VWA.
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Magnesium. 1 17
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Pfam; PF01839; FG-GAP;
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STRAIN-WHITE LEGHORN;

MEDLINE-92011862; PubMed=1918137;

Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,

Nishida Y., Obara M., Kimata K.,

"The complete primary structure of type XII collagen shows a chimeric

"The complete primary structure of type XII collagen shows a chimeric
molecule with reiterated fibronectin type III motifs, von Willebrand
molecule with reiterated fibronectin type III motifs, von Willebrand
factor A motifs, a domain homologous to a noncollagenous region of
type IX collagen, and short collagenous domains with an Arg-Gly-Asp
site.":
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                       66 IIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLAR-----IADSKDH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-1283 FROM N.A. (SHORT FORM), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                            11 TTLMKLJEDREQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYENRQGYRTA-SV 65
                                                                                                                                                                                                                                                                                          18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 VFKV-DNFAALGSIQKQLQEK----IYAVEGTQSRASSSFQHEMSQEGFSTALTMD 362
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. (POTENTIAL)
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"Type XII collagen: distinct extracellular matrix component discovered by cDNA cloning."; 84:6040-6044(1987).
                                                                                                                                                                                                                             Query Match 10.1%; Score 114; DB 1; Length 1162; Best Local Similarity 27.3%; Pred. No. 0.043; Matches 48; Conservative 27; Mismatches 83; Indels 18
                                                                                            L -> V (IN REF. 2).
V -> A (IN REF. 2).
W, F296AlA35455D77D CRC64;
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P13944; O04509;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
COllagen alpha 1(XII) chain precursor (Fibrochimerin).
   MISSING (IN REF. 2).
GHPW -> ATP (IN REF. 2).
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MEDLINE=93042014; PubMed=1420368;
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MEDLINE=87317590; PubMed=3476925;
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[2]
                                                                                                                                                         126885 MW;
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ITAM_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
ALTERNATIVE SPLICING.

MEDLINE-95370352; PubMed-7642694;

MEDLINE-95370352; PubMed-7642694;

MICOLINE-95370352; PubMed-7642694;

MICOLINE-95370352; PubMed-7642694;

"Large and small splice variants of collagen XII: differential expression and ligand binding.";

OCHI BIOL. 130:1005-1014(1957).

-I- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE SURRACE OF THE FIBRILS. AND THE COLL AND NC3 DOMAINS MAY BE LOCALIZED IN THE PERIFIBRILLAR MATRIX.

-I- SUBUNIT: TRIMER. OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: THIS SEQUENCE DEFINES FIRE DISTINCT DOMAINS, TWO TRIPLE-
HELICAL DOMAINS (COL1 AND COL2) AND THREE NONTRIPLE-HELICAL
HELICAL NC1, NC2, AND NC3).
PUMAINS (NC1, NC2, AND NC3).
EACH END.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-x-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PTM: GLYCOSYLATED, CHONDROITIN'SULFATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY. SIMILARITY: CONTAINS 4 VWFA DOMAINS. SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS, LIGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE TISSUES CONTAINING TYPE I COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLLAGEN ALPHA 1(XII) CHAIN. FIBRONECTIN TYPE-III 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWFA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000087; Collagen.
InterPro: IPR003961; FN III.
InterPro: IPR003962; FNIII_repeat.
InterPro: IPR003129; TSPN.
InterPro: IPR002035; vWFA.
                                                                                                                                                                                                                                                                    NONTRIPLE-HELICAL SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, D00824, BAA00701.1, --
EMBL, X1024; BAA48718.1, --
EMBL, M17375, AAA48718.1, --
EMBL, J05137; AAA4873.1, --
EMBL, X67327; CAA47744.1, --
PIR, A34485, A34485.
HSSP, P17301, 1AOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0014; FNTYPEIII.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 17.
SMART; SM00310; TSPN; 1.
SMART; SM00327; VWA; 4.
PROSITE; PS50234; VWFA; 4.
Extracellular matrix; Connect:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01391; Collagen; 4. Pfam; PF00041; fn3; 17. Pfam; PF02210; TSPN; 1. Pfam; PF00092; vwa; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3124
3124
114
311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 AIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPST 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSEREANRSRDLG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO CHOUNCOITIN SULEATE (POTENTIAL).
TO CHOUNCOITIN SULEATE (POTENTIAL).
TO CHONDROITIN SULEATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                         NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                           NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3076 QP -> AG (IN REF. 3).
AA; 340578 MW; 094285AFE7F346CF CRC64;
                                                                                                                                                 FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-III 11.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 13.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 16.
                                ASP/GLU-RICH (ACIDIC).
ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLSK 190
                                                                                FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T -> S (IN REF. 4).
D -> E (IN REF. 4).
P -> A (IN REF. 2).
L -> F (IN REF. 2).
V -> F (IN REF. 2).
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :|:|:||:||:||:|----EQELAAIRKKSYVPAKNMVFSDVTSDSFKVSWSAAGSE
                                                FIBRONECTIN
FIBRONECTIN
                                                                                                                                                                                                                                                                                                                              VWFA 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Conservative
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3048
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NATULE 314:540-542(1985).

-1. FUNCTION: INTEGRAN ALPHA-MARTA-2 IS IMPLICATED IN VARIOUS
ADHESTVE INTEGRAN ALPHA-MARTA-2 IS IMPLICATED AND GRANULOCYTES
AS WELL AS IN MEDIATING THE UPTAKE OF COMPLEMENT-COMPED PARTICLES.
IT IS IDENTICAL WITH CR-3, THE RECEPTOR FOR THE IC38 FRAGMENT OF
THE THIRD COMPLEMENT COMPONENT: IT PROBABLY RECOGNIZES THE R-G-D
THE THIRD COMPLEMENT COMPONENT: IT PROBABLY RECOGNIZES THE R-G-D
FEDRINGEN, FACTOR X AND ICAMI. IT RECOGNIZES PLAN AND PEPTIDES
FIBRINGGEN GRAMA CHAIN ALPHA-M/BETA-2 PLAY A CRITICAL ROLE IN
GLOMERILONEPHRITIS. MICE EXPRESSING A NULL MATION OF THE ALPHA-M
GLOMERILONEPHRITIS. MICE EXPRESSING A NULL MATION OF THE ALPHA-M
RESPONSE TO A IMPAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT
RESPONSE TO A IMPAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH LOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                           01-NOV-1988 (Rel. 09, Created)
01-REB-1991 (Rel. 17, Last sequence update)
01-MRA-2002 (Rel. 41, Last annotation update)
11-MRA-2002 (Rel. 41, Last annotation update)
11-tegrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
                                                                                                                                                                                                                                                                                                                          "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with eintegrin family and an additional domain related to von Willebrand factor.";
EMBO J. 7:1371-1378(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALDS/C; TISSUE-Spleen;
MEDIJINE-86287312; PubMed-2942940;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
"A partial genomic DNA clone for the alpha subunit of the mouse
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSOCIATES WITH BETA-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Springer T.A., Teplow D.B., Dreyer W.J.; Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon."; Nature 314:540-542(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 17-28.
MEDLINE=85188276; PubMed=3887182;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88312584; PubMed=3044779;
                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 11-45 FROM N.A.
STANDARD;
                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRANULOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBESIT
  ITAM_MOUSE
                                                                                                                                                                                                                                                                                                                      Pytela R.;
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94 AIVYCVGVKD-FNETQLARIAD-----SKDHVFPVNDGFQALQGIIHSILKKSCIEILA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 VIRYVIGVGNAFNKPQSRRELDTIASKPAGEHVFQV-DNFEALNTIQNOLQEK----IFA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 GDTYMHEGFERASEQIYYE-NRQCYRTASVIIALTDGELHEDLFFYSE--REANRSRDLG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Gaps
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(POTENTIAL).
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                                           PRINTS, PROLIS, INTEGRINA.
PRINTS, PROLISS, INTEGRINA.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 112; DB 1; Length 1153;
29.1%; Pred. No. 0.064;
tive 26; Mismatches 56; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                         178DB988AECB0343 CRC64;
                                                                                                                           INTEGRIN ALPHA-M.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
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(GLCNAC. ..)
(GLCNAC. ..)
(GLCNAC. ..)
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FG-GAP 6.
FG-GAP 7.
POTENTIAL.
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FG-GAP 2.
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                                                                                                                                             POTENTIAL
                                                                                                                                                                                      FG-GAP
   InterPro: IPR000413; Integrin_alpha. InterPro: IPR002035; vWFA. Pfan; PF0183; FC-6AP; 5. Pfan; PF00357; integrin_A; 1. Pfan; PF00092; vwa; 1.
                                                                                                                                                              FG-GAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 127480
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                                                                                                            Signal; Calcium; Repeat.
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7111
776
1023
1033
58
391
696
734
772
801
8811
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1153
1105
1129
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MGD; MGI:96607; Itgam.
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Best Local Similarity
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1106
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EMBL; X07640; CAA30479.1; -. EMBL; M14293; AAA39484.1; -. PIR; S00551; S00551. HSSP; P11215; IABX.

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EMBL;
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Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.; "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins."; Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93123748: PubMed-8419480;
Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
"Structural analysis of the Collb gene and phylogenetic analysis of
the alpha-integrin gene family demonstrate remarkable conservation of
genomic organization and suggest early diversification during
                                                          01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1)
ITGAM OR CR3A OR CD11B.
                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=88315033; PubMed=2457584;

Gorbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;

"The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD1lb) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";

J. Biol. Chem. 263:12403-12411(1988).
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-88257215; PubMed-2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Annio acid sequence of the alpha subunit of human leukocyte adhesion
receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits."; Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 9-1153 FROM N.A.
MEDLINE-89098893; Pubmed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shelley C.S., Arnaout M.A.; "The promoter of the CD11b gene directs myeloid-specific and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92144986; PubMed-1346576;
Pahll H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                       PRT; 1152 AA
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MEDLINE-87076671; PubMed=3539202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92073318; PubMed-1683702;
                                                (Rel. 11, Created)
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                       STANDARD;
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                                                                                                                                                                       NCBI_TaxID=9606;
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                                              01-JUL-1989
                      ITAM_HUMAN
P11215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roth G.J.;
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          ITAM_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd11b.htm".
                                                                                                                                                                  Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin
                                                                                                                                                                                                                                                                                                                                                              Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.; "Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
MEDLINE-98362595; PubMed-9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks W.B., Finzel B.C., Mider R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Midner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
"N-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa."; Biochim. Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE-963631; PubMed-8747460;
                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure 3:1333-1340(1995).
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AAB24821.1;
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                                                                                                                                                                                                                           CR3 (CD11b/CD18).";
Cell 80:631-638(1995).
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S52153;
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S52155;
S52157;
S52159;
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Collagen; Glycoprotein.
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154
245
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                                                                                                     NCBI_TaxID=8316;
            CAIC_NOTVI
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     CA1C_NOTVI
                       7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 VIRYVIGVGDAFKSEKSRQELNTIASKPPRDHVFQVNN-FEALKTIQNQLREK----IFA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                nterpro; IPR000413; Integrin_alpha.

Interpro; IPR002035; vWFA.

Interpro; IPR002035; vWFA.

Pfam; PF01839; FG-GAP; 5.

R pfam; PF00183; INTEGRINA.

R PRINTS; PR01185; INTEGRINA.

R PRINTS; PR01915; INTEGRINA.

R SMART; SM00191; INTEGRINA.

R SMART; SM00191; INTEGRIN_ALPHA; 1.

R PROSITE; PS00242; INTEGRIN_ALPHA; 1.

R PROSITE; PS50234; VWFA; 1.

R PROSITE; PS10234; VWFA; 1.

R PROSITE; PS10242; INTEGRIN_ALPHA; 1.

R PROSITE; PS10244; INTEGRINA; INTEGRINA.

R SIGNAL .

I 1.16
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CYTOPLASMIC (POTENTIAL)
FG-GAP 1.
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  S52164, AAB24821.1; JOINED.
S52165, AAB24821.1; JOINED.
S52167, AAB24821.1; JOINED.
S52170, AAB24821.1; JOINED.
S52173, AAB24821.1; JOINED.
S52173, AAB24821.1; JOINED.
S52180, AAB24821.1; JOINED.
S52181, AAB24821.1; JOINED.
S52181, AAB24821.1; JOINED.
S52189, AAB24821.1; JOINED.
S52189, AAB24821.1; JOINED.
S52192, AAB24821.1; JOINED.
S52192, AAB24821.1; JOINED.
S52213; AAB24821.1; JOINED.
S52213; AAB24821.1; JOINED.
S52213; AAB24821.1; JOINED.
S52213; AAB24821.1; JOINED.
S52213; AAB24821.1; JOINED.
S52213; AAB24821.1; JOINED.
S52221; AAB24821.1; JOINED.
S52222; AAB24821.1; JOINED.
                                                                                                                                                                                                           M76724; AAA58410.1; -. M84477; AAA51960.1; -. A31108; RWHUIB. A26091; A26091;
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CONTINUE STANDARD: PRT; 929 AA.

COLIAGO 116. 136. Created)

DT 11-111-1996 (Rel. 13. Details Sequence update)

DT 11-111-1996 (Rel. 14. Last sequence update)

DT 11-111-1996 (Rel. 14. Last sequence update)

COLIAGO 1140 1471 (ALC) Adail (Fragmench) (Triturus viridescens).

SOS (COLIAGO 1140 1471) Adail (Fragmench) (Triturus viridescens).

SOS (COLIAGO 1140 1471) Adail (Fragmench) (Triturus viridescens).

SOURCE FROM N.A. Detail (Architect Salamandridae: Architect Sa
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BINDING
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  1. Dev. Dyn. 204:432-445(1995).

1. Dev. Dyn. 204:432-445(1995).

2. -! FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBELIES, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBELIES, AND THE COL2 AND NG3 DOMAINS MAY BE
LOCALIZED IN THE PERIFIBRILAR MATRIX (BY SIMILARITY).

2. -! SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF
NOWTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).

2. -! ALTERNATIVE PRODUCTS: 2 ISOPRAMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM OF COLLAGEN XII MAY CONTAINING 190 KDA OF EITHER THE LONGER
COR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT
CORN CHAINS. ONLY THE LONG VARIANT IS A PROTECCLYCAN.

2. ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTECCLYCAN.

3. SKIN, CORNEA, SCLERA, BLOOD VESSELS, AND PERIOSTEUM.

3. SKIN, CORNEA, SCLERA, BLOOD VESSELS, AND PERIOSTEUM.

3. SKIN, CORNEA, SCLERA, BLOOD VESSELS, AND 11); AT LATER STAGES OF
DEVELOPMENTAL STAGE: LONG FORM OF COLLAGEN XII, XIIA, IS THE
PREDOMINANT FORM AT EARLY STAGES (ED7 AND 11); AT LATER STAGES OF
DEVELOPMENT (ED15 AND 17) THE SHORT FORM, XIIB, BECOMES THE MAJOR
PRODMINANT FORM AT EARLY STAGES (ED7 AND 11); AT LATER STAGES OF
CORNELLOPMENT (ED15 AND 17) THE SHORT FORM, XIIB, BECOMES THE MAJOR
CONTAINING THE SHORT FORM BECOMES THE MAJOR PRODUCT, THE LONG SPLICE
CONTAINUNES TO BE EXPRESSED IN SEVERAL TISSUES, EVEN AFTER
                                                                                                                                                                                8
                                                                                                                                                                                                                                                                       655 FISRVVEVFDIGSDRVQIAVSQYSGDPRTEWQLNTHKTKKSLMDAVANLPYKGGNTNTGS 714
                                                                                                                                                                                                                                                                                                           100 GVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSILKKSCIEILAA----EPSTICA 154
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STATAR-WANTSS WEBSTER, AND C57BL/61; TISSUB-Skin;
MEDLINE-96170761; PubMed-8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic development."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                        44 GFERASEQIYYENRQGY----RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCV
                                                                (POTENTIAL).
             VWFA 2.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
                                                                                                                                                                                42;
                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                       Score 109; DB 1; Length 929;
Pred. No. 0.09;
                                                                                                                                                                               73; Indels
                                                                                                                 101647 MW; AE5D7485254FD954 CRC64;
  FIBRONECTIN TYPE-III 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                     Query Match
9.6%; Score 109; DB
Best Local Similarity 24.2%; Pred. No. 0.09
Matches 46; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                          907
>929
231
324
415
98
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(Rel. 36, 1
(Rel. 41, 1
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929 AA;
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                                                                            415
98
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15-JUL-1998
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Q60847;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R InterPro; IPR003129; TSPN.
R InterPro; IPR003129; TSPN.
R InterPro; IPR003129; TSPN.
R Pfam; PF00139; Collagen; 4.
R Pfam; PF00139; Vwa; 4.
R Pfam; PF00014; FWA: 18.
R PRINTS; PR00014; FWA: 16.
R SMART; SM00210; TSPN; 1.
R SMART; SM00217; VWA; 4.
R SMART; SM00317; VWA; 4.
R PRINTS; PS50334; VWFA; 4.
R PROSITE; PS50334; VWFA; 4.
R PROSITE; PS50334; VWFA; 4.
R PROSITE; PS5034; VWFA; 4.
R PRO
PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).
                                                                             -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NONHELICAL REGION (NC1).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
                                                                                                                                                              SIMILARITY).
-!- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
-!- SIMILARITY: COWTAINS 4 WWFA DOMAINS.
-!- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRIPLE-HELICAL REGION (COL2)
WITH I IMPERECTION.
NONHELICAL REGION (NC2).
WITH 2 IMPERFECTIONS.
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FIBRONECTIN TYPE-III 10
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
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FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
FIBRONECTIN TYPE-III 9
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FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
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InterPro; IPR000087; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FNIII_repeat.
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PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00134; TRYPSIN_HIS;
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R EMBL; M60577; AAA37381.1; JC
R EMBL; M60578; AAA37381.1; JC
EMBL; M57891.1; JC
PIR; A38876; C2MS;
HSSP; P00757; 1SGF.
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M60568;
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M60573;
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M60605;
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M60565;
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M60568;
M60569;
M60570;
M60571;
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M60572;
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M60605;
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                                                                         PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 LKKSCI-----EILAAE----PSTICAGESFQVVVRGNGFRHARNVDRVLCSFKIND 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 REDLLAAVKKIPYKGGNTMIGDAIDYLVKNIFTESAGSRAGFPKVGIII--TDGKSQDEV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 9.6%; Score 109; DB 1; Length 3067;
1 Similarity 22.8%; Pred. No. 0.38;
51; Conservative 38; Mismatches 69; Indels 66; Gaps
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  TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-SING (GLNAC. ...) (POTENTIAL).
MISSING (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
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Mus musculus (Mouse).
Mus musculus (Mouse).
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1991 (Rel. 18, Created)
1-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
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SEQUENCE
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                                              Plasma; Glycoprotein; Hydrolase; Serine protease;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
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                                                                 Sushi; Alternative splicing
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099715; 099716;
15-JUL-1998 (Rel. 36, Created)
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01-MAR-2002 (Rel. 41, Last annotation u
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PROSITE; PS00135; TRYPSIN_SER; 1.
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Best Local Similarity 24.3%
                       PROSITE; PS50234; VWFA; 1.
Complement pathway; Plasme
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      NONTRIPLE-HELICAL SEQUENCES.
-1 ALTERNATIVE PRODUCES: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTECCIVCAN.
-1 TISSUE SPECIFICITY: FOUND IN COLLAGEN I-CONTAINNG TISSUES: BOTH SHORT AND LONG ISOFORMS APPEAR IN AMNION, CHORION, SKELETAL MUSCLE, SMALL INTESTINE, AND IN CELL CULTURE OF DERMAL FIBROBLASTS, KERATINOCYTES, AND ENDOTHELIAL CELLS. ONLY THE SHORT ISOFORM IS FOUND IN LUNG, PLACENTA, AND A SQUAMOUS CELL CARCINOMA CELL LINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY.
-!- SIMILARITY: CONTAINS 4 VWFA DOMAINS.
-!- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                           PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EACH END (BY SIMILARITY).
-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
   splice variants of collagen XII,
                                                                                                                                                                                                                                                                                              LOCALIZED IN THE PERIFIBRILLAR MATRIX (BY SIMILARITY).
-!- SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kba of
"Complete primary structure of two splice variants of collagen X and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX) collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human chromosome 6q12-q13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00060; FN3; 17.
SMART; SM00210; TSPN; 1.
SMART; SM00217; VWA; 4.
PROSITE; PS50244; VWRA; 4.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLLAGEN ALPHA 1(XII) CHAIN
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FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 7
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InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
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Interpro: IPR002129; TSPN.
Interpro: IPR002139; VWFA.
Pfam; PF02110; Collagen; 4.
Pfam; PF02210; TSPN; 1.
Pfam; PF00012; VWA; PRINTS; PR00014; FNTYPEIII.
PRINTS; PR000143; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U73778; AAC51244.1; -. EMBL; U73779; AAD40483.1; -.
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"PUTILICATION and alpna subunit N-Terminial sequences of number of an additional made of an additional made of an additional made of an additional made of a language of leukocyte addesion proteins.";

"I Immunol. 1381-2383 (1987)

"I Immunol. 1381-2383 (1987)

"I FUNCTION: INTEGRIN ALPHA-X/BETA-2 IS A RECEPTOR FOR FIBRINOGEN. IT RECORDINES THE SEQUENCE G-PR IN FIBRINOGEN. IT MEDIATES CELL-CELL INTEGRINATION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY

"INFORTANT IN MONOCYTE ADHESTON AND CHEMOTARIS."

"INFORTANT HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-X ASSOCIATES WITH BETA-2.

"ISOBCELLULAR LOCATION: Type I membrane protein. MONOCYTES AND GRAULOCYTES.

"ISOBCELLULAR IN THE INTEGRIN IN TOWAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS OF THE INTEGRIN ALPHA CHAIN FAMILY.

"IT ISOBCELLARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

"INTERATITY: CONTAINS 7 FG-GAP REPEATS.

"ISIMILARITY: CONTAINS 7 FG-GAP REPEATS.

"ISIMILARITY: CONTAINS 7 FG-GAP REPEATS.

"INTERALITY: CONTAINS 7 FG-GAP REPEATS.

"INTERALITY: NAME-PROM; NOTE-CD guide CD11c entry;

WWW—"http://www.ncbi.nlm.nlm.nlm.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                MEDLINE-8816645; PubMed=3327687; MEDLINE-8816645; PubMed=3327687; Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; Corbi A.L., Maller Complete primary structure of the alpha subunit of "cDN cloning and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 20-43.
MEDLINE-8716/7596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1ntegrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu M5).
ITGAX OR CD11C.
                                                                                                                                       Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.";
J. Biol. Chem. 265:2782-2788(1990).
                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
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EMBL; M29487; AAA51620.1; ALT_SEQ.
EMBL; M29483; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
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HSSP; P11215; 1A8X.
CarbBank; CCSD:33581;
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                                                                                                                                                                                                                                                                                        NATIH LITERAREACHION.
NONHEDICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
WHITH 2 IMPEREBETIONS.
NONHEDICAL REGION (NC1).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
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NONHELICAL REGION (NC3)
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FIBRONECTIN TYPE-III 10
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FIBRONECTIN TYPE-III 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 RQGYRTAS-VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV-----KDFN 105
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                                                                                                                                                                                                                             PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA:
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
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EXTRACELLULAR (POTENTIAL).
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FG-GAP 2.
WWFA.
WG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 7.
POTENTIAL.
POTENTIAL.
POTENTIAL.
GFFKR MOTIF.
                                                                               InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Magnesium; Calcium; Repeat.
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                                                                                                                                             Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
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1163 AA;
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-:- SUBURIT: HOMOTRIMER (PROBABLE).
-:- SUBURIT: HOMOTRIMER LOCATION: Extracellular matrix.
-:- SUBCELLULAR LOCATION: Extracellular matrix.
-:- STREET SCONNECTIVE TISSUE DISTRIBUTION; HIGH PRESENCE IN DENSE CONNECTIVE TISSUE IN SKELETAL MUSCLE.
-:- PTW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-x-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-:- PTW: MAY CONTAIN CYSTEINE RESIDUES INVOLVED IN INTER- AND INTRAMOLECULAR DISULATIDE BONDING.
-:- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTRRUPLECTULAR DISULATIDE PAMILS.
-:- SIMILARITY: CONTAINS 2 WAFA DOMAINS.
-:- SIMILARITY: CONTAINS 2 WAFA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99280705; PubMed-10350466; MoLeish M.J., Hill J.M., Ficheux D., Montserret R., Aubert-Foucher E., McLeish M.J., Penin F.; Jaquinod M., van der Rest M., Deleage G., Penin F.; Jactinod M., van der Rest the heparin binding site of the NC1 domain of Structural analysis of the heparin binding site of the NC1 domain of
                                                       01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
020114A1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Biochemistry 38:6479-6488(1999).
-!- FUNCTION: AN ADHESIVE ROLE BY INTEGRATING COLLAGEN BUNDLES. IT I PROBABLY ASSOCIATED WITH THE SURFACE OF INTERSTITIAL COLLAGEN FIBRILS VIA COLI. THE COL2 DOMAIN MAY THEN SERVE AS A RIGID ARM WHICH STICKS OUT FROM THE FIBRIL AND PROTRUDES THE LARGE N-TERMINAL GLOBULAR DOMAIN INTO THE EXTRACELLULAR SPACE, WHERE IT MIGHT INTERACT WITH OTHER MATRIX MOLECULES OR CELL SURFACE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                      Waelchii C., Trueb J., Ressler B., Winterhalter K.H., Trueb B.; "Complete primary structure of chicken collagen XIV."; Eur. J. Biochem. 212:483-490(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 402-1549 FROM N.A.
MEDIINE-92339443; PubMed=1339349;
Trueb J., Trueb B.;
Trype XIV collagen is a variant of undulin.";
Eur. J. Blochem. 207:549-557(1992).
PRT; 1888 AA.
                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
MEDLINE=93185668; PubMed=8444186;
                                          01-JUL-1993 (Rel. 26, Created)
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  STANDARD;
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PDB; 189Q; 25-FEB-99
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                Gallus.
NCBL_TaxID=9031;
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InterPro; IPR000087; Collagen.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
MA. 39915BB9F46DD873 CRC64;
                                                                                                                                                                                                                                      tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1888;
                                                                                                                                   PRINTS; PRO0014; PRITYPEIII.
PRINTS; PR000153; VWFADOMAIN.
SMART; SM00060; FN3; 7.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 2.
PR0STEF; PS50234; VWFA; 2.
PR0STEF; PS50234; VWFA; 2.
CEXTRACELLULAR MALLIX; COnnective tissue; Repeat; Hydroxylatic cell adhesion; Collagen; Glycoprotein; Signal; 3D-structure.
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VWFA 1.
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
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TRIPLE-HELICAL REGION 1.
TRIPLE-HELICAL REGION 2.
POLY-THR.
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22.5%; Pred. No. 0.77;
iive 36; Mismatches 98;
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01-MAY-1991 (Rel. 18, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Cartilage matrix protein precursor (Matrilin-1).
MATALIOR CRTW OR CMP.
Homo sapiens (Human).
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                 InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003129; TSPN.
InterPro; IPR02035; VWFA.
Pfam; PF01391; Collagen; 4.
Pfam; PF02041; fn3; 8.
Pfam; PF02210; TSPN; 1.
Pfam; PF02210; TSPN; 1.
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          InterPro; IPR003961; FN_III
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Best Local Similarity
Matches 49; Conserv
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SEQUENCE FROM N.A.
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1664
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P21941;
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CARBOHYD
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CAMA_HUMAN
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PRINTE; PRO0453; VWFADOMAIN.

SMART; SM00181; BGF.

SMART; SM001827; VWA: 2.

PROSITE; PS010186; BGF.2; 1.

PROSITE; PS01186; BGF.2; 1.

BROSITE; PS01186; BGF.2; 1.

BROSITE; PS010186; BGF.3; 1.

BGF.11ke domain; Signal; Glycoprotein; Cartilage; Repeat; Coiled coil.
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MEDLINE-91060568; PubMed-2246248;
Jenkins R.N., Osborne-Lawrence S.L., Sinclair A.K., Eddy R.L. Jr
Byers M.G., Shows T.B., Duby A.D.;
Structure and chromosomal location of the human gene encoding
cartilage matrix protein."
J. Biol. Chem. 265:19674-19631(1990).
FUNCTION: CARTILAGE MATRIX PROTEIN IS A MAJOR COMPONENT OF T
EXTRACELIULAR MATRIX OF NONARTICULAR CARTILAGE. IT BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2D880A8114C7940F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARTILAGE MATRIX PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.5%; Score 96.5; DB
29.7%; Pred. No. 0.51;
Live 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                            -i-SUBBNIT: HOMOTRIMER.
-i-SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i-SIMILARITY: CONTAINS 2 VWFA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWFA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-like.
InterPro; IPR002035; vWFA.
Pfam; PF00008; EGF; 1.
Pfam; PF00092; vWa; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STICAGES --- FQVVVRG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
263
453
495
76
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTAINING FIBRILS, THE COLI DOMAIN COULD BE ASSOCIATED WITH THE SURFACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE LOCALIZED IN THE PERIFIBILAR MATRIX (BY SIMILARITY).

SUBUNIT: TRIMER OF IDEMTICAL CHAINS EACH CONTAINING 190 KDa OF NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).

PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
--- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
--- INTERRUPTED HELICES (FACIT) FAMILY.
--- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR00361; FN_III.
InterPro; IPR00361; FN_III.
InterPro; IPR002035; vwFa.
InterPro; IPR000035; vwFa.
SMART; SM00060; FN3; 5.
SMART; SM00060; FN3; 5.
ENART; SM00377; vwA; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell mather Collagen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhan Q., Burrows R., Cintron C.; "Localization of type XII collagen in normal and healing rabbit cornea by in situ hybridization."; Exp. Eye Res. 60:551-561(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71032 MW; 162C6A923F551E6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III 6.
                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain (Fragment).
                                                                    639 AA
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95339912; PubMed-7615021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S78179; AAB34889.2; -. HSSP; P02751; 1TTF.
                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Cornea
                                                                 CA1C_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
RESULT 15
CA1C_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>-</u>
                                                                                            SOUTH THE THE THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE TENT THE
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6

Gaps

24;

8.4%; Score 95; DB 1; Length 639; 26.1%; Pred. No. 0.93; Live 29; Mismatches 60; Indels

Best_Local Similarity 26.18 Matches 40; Conservative

Query Match

Search completed: August 9, 2002, 10:47:09 Job time: 832 sec

LTINLCNSVKGPGDLEAPSNLVISERTHRSFRV 146

Fri Aug

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

August 9, 2002, 10:34:21; Search time 61.73 Seconds Run on:

(without alignments)
339.340 Million cell updates/sec

Title: Perfect score:

US-09-970-076-10 1131 1 MSFIVFSTRGTTLMKLTEDR......STSGFKEGNSHPCLPARPHT 218 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database

pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
٦	114	10.1	3124		A40020	collagen alpha 1(X
7	112	9.9	1153	7	800551	leukocyte surface
٣	111	9. 8.	1153	٦	RWHU1B	cell surface glyco
4	109.5	9.7	1747	۲	A45974	iqen alpl
S	109	9.6	929	N	151027	
Q	106.5	9.4	160	П	C2MS	
7	105.5	9.3	724	7	A48569	antiqen Em100 - Ei
æ	103	9.1	1163	7	RWHU1C	cell surface glyco
6	102.5	9.1	1857	~	S31212	collagen alpha 1(X
10	102.5	9.1	1888	~	S78476	collagen alpha 1(X
11	66	8.8	869	~	B96958	dnaK protein (heat
12	96.5	80.5	496	N	A37979	cartilage matrix p
13	96.5	.5 .5	817	~	T50240	kinesin-like prote
14	95	8.4	764		ввни	complement factor
15	93.5	8.3	200	7	866522	cartilage matrix p
16	92.5	8.2	4307	~	T20721	hypothetical prote
17	06		712	ď	A45638	immunodominant mic
18	88	•	537	~	T04822	hypothetical prote
19	89	7.9	843	7	A40970	undulin 1 - human
20	88.5	•	487	Н	VZEBPT	sensor kinase phog
21	88	7.8	2944	~	A54849	collagen alpha 1(V
22	87	•	689	7	F84811	probable retroelem
23	9		487	~	AG0646	sensor protein Pho
24	85.5	7.6	453	7	н96798	hypothetical prote
25	S	7.6	3176	7	CGHU3A	ᇨ
56	82	7.5	3051	7	S42373	hypothetical prote
27	84.5	7.5	237	7	E69838	transcription regu
28	84.5	7.5	240	7	G71227	hypothetical prote
59	83.5	7.4	432	-	E70373	<u></u>

hypothetical prote hypothetical prote	transcription regu conserved hypothet	hypothetical prote hypothetical prote	comprement factor hypothetical prote	hypothetical prote penicillin-binding	hypothetical prote pentcillin-binding	penicillin-binding penicillibinding p	DNA polymerase I - spore coat peptide	•
T21280 T51512	AF1166 B71257	A86351 D59092	BBMS T13530	T19173 S16629	AG2285 F95039	S06726 H97909	F71816 H69605	
77	00	77	7 7	~ ~	0 0	77	0 0	1
1107 273	334	230	853	1027	710	750	189	
7.4	7.3	 	 	7.3	2.7	7.2	2.7	
83.5	82.5 82.5	82.5 82	8 8 8 8	81.5	81.5 81.5	81.5	81.5	1
30 31	332	35	37	80 O F) F)	404	4 4 3 8	4 4 5	:

ALIGNMENTS

	RESULT I
	A40020
	collagen alpha 1(XII) chain precursor - chicken
	N; Alternate names: fibrochimerin
	C;Species: Gallus gallus (chicken)
	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
	C; Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
	R;Yamaqata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; O
	J. Cell Biol. 115, 209-221, 1991
	A; Title: The complete primary structure of type XII collagen shows a chimeric molecul
	nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp si
	A; Reference number: A40020; MUID:92011862
_	A;Accession: A40020

Accession: S23814 A; Molecule type: protein A; Residues: 'X', '1333, '0', '1335-1347; 1914-1928; 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-251 B; Dublet, B.; wan der Rest, M. J. Biol. Chem. 262, 17724-17727, 1987 A; Title Type vir collagen is expressed in embryonic chick tendons. Isolation of peps A; Reference number: S22254; MUID: 88087065 A; Accession: S22254 A; Residues: 2831-2832, T', 2834, 'R', 2836-2843; 3002-3014 <DUB>
R; Trueb, J; Trueb, B.;

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A; Accession: A31108
A; Accession: A31108
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Corss-references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Cross-references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Note: part of this sequence was confirmed by protein sequencing
B; Arnaout, M.A; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
B; Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion recepto
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion recepto
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion recepto
A; A; Molecule type: Muld: Mul
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                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA A; Residues: 1-1153 <PTY>
A; Residues: 1-1153 <PTY>
A; Residues: 1-1153 <PTY>
A; Residues: 1-1153 <PTY>
A; Residues: 1-1153 <PTY>
A; Residues: EMBL: X07640; NID: 952982; PIDN: CAA30479.1; PID: 952983
A; Cross-references: EMBL: X07640; NID: 952982; W.J.; Gee, C.E.; Larson, R.S.; Rober R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Droger, W.J.; Gee, C.E.; Larson, R.S.; Rober R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Droger, W.J.; Gee, C.E.; Larson, R.S.; Rober R; Sastre, L.; Roman, J.M.; Teplow, S. 5644-5649, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement re A; Reference number: 159078; MUID: 86287312
A; Reference number: 159078
A; Retering preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                         A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with th A;Reference number: S00551; MUID:88312584
A;Accession: S00551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ajdene: Mac-1
C; Superfamily: cell surface glycoprotein CDilb; von Willebrand factor type A repeat h
C; Superfamily: cell adhesion; glycoprotein; transmembrane protein
C; Keywords: cell adhesion; glycoprotein; predicted <SIGS
F;1-15/Domain: signal sequence #status predicted <SIGS
F;17-1153/Product: leukcoyte surface glycoprotein Mac-1 alpha chain #status experimen
F;148-318/Domain: von Willebrand factor type A repeat homology <WMA2>
F;1106-1129/Domain: transmembrane #status predicted <PWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 VIRYVIGVGNAFNKFQSKRELDTIASKPAGEHVFQV-DNFEALNTIQNQLQEK----IFA 334
                                                      22-0ct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDTYMHEGFERASEQIYYE-NRQGYRTASVIIALIDGELHEDLFFYSE--REANRSRDLG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 112; DB 2; Length 1153; 29.1%; Pred. No. 0.14; ative 26; Mismatches 56; Indels 11
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change
C;Accession: S00551; I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-499,501-965,'P',967-1153 <ARN>
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Best Local Similarity 29.1
Matches 41; Conservative
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EMBO J. 7, 1371-1378, 1988
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A. Thtron. 2865/3; 2867/3; 2867/3; 2869/3; 2869/3; 2922/1; 2985/1; 3008/1; 3008/1

C. Superfamily, colladen alpha I(XII) chain status predicted connective tissue; disulfice (Superfamily, Colladen alpha I(XII) chain status predicted connective tissue; disulficed (Superfamily, Colladen alpha I(XII) chain status predicted connective tissue; predicted connective tissue; disulficed (Superfamily, Colladen alpha I(XII) chain status predicted connective tissue; predicted connective tissue; disulficed connective tissue; predicted connective tissue; display connective tissue; display connective tissue; predicted connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective tissue; display connective 
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                                                      Biochim. Biophys. Acta 1171, 97-98, 1992
A;Title: The two splice variants of collagen XII share a common 5'
A;Reference number: S28811; MUID:93042014
A;Accession: $28811
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                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-24/1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
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Best Local Similarity 27.8
Matches 45; Conservative
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Astrocession: A45974; NUID:93280195
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N.Alternate names: undulin
C.Species: dallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A45974; S30085; S22916; S17035; S20833
R.Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' reg
                        F;1135-1153/Domain: intracellular #status predicted <INT>
F;86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 AIVYCVGVKDFNETQLAR-----IADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 GDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHEDLFFYSE--REANRSRDLG
                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                      Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                      27; Mismatches
                                                                                                                                                                                                          Query Match 9.8%; Score 111; Best Local Similarity 28.5%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                41; Conservative
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A; Map position: 16pl1.2-16pl1.2
A; Note: promoter contains a GATA moutif and two Spl consensus binding sites
A; Note: promoter contains a GATA moutif and two Spl consensus binding sites
C; Superfamily: cell surface glycoprotein CDID; von Willebrand factor type A repeat home
C; Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C; Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C; Keywords: alternative splicing; predicted <SIG>
F; 1-16/Domain: signal sequence #status predicted <SIG>
F; 1-1183/Poomain: extracellular #status predicted <SIG>
F; 148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F; 148-318/Domain: calcium/magnesium binding #status predicted
F; 530-538/Region: calcium/magnesium binding #status predicted
F; 533-601/Region: calcium/magnesium binding #status predicted
F; 1109-1134/Domain: transmembrane #status predicted <TWM>
A;Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594 A;Note: the authors translated the codon TAC for residue 1129 as Thr A;Note: part of this sequence, including the amino end of the mature protein, was confir R;Shalley, C.S.; Arnaout, M.A. Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991 A;Title: The promoter of the CD11b gene directs myeloid-specific and developmentally reg A;Reference number: A41600; MUID:92073318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 9-1153 <HIC.>
A; Cross-references: GB.J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross-references: GB.J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Note: part of this sequence was confirmed by protein sequencing
R; Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
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A:Status: not compared with conceptual translation
A:Status: not compared with conceptual translation
A:Residues: 1-499,501-1153 <FLE>
A:Residues: 1-499,501-1153 <FLE>
A:Residues: 1-499,501-1153 <FLE>
A:Cross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A:Cross-references: GB:S52227; NID:g263047; A:Rote: sequence extracted from NCBI backbone (NCBIP:121963)
B:Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Bacchim. Blophys. Acta 874, 368-371, 1986
A:Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across spacession: A26091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
A;Tetle: CDNA sequence for the alpham subunit of the human neutrophil adherence receptor A;Reference number: A3218; MUID:89098893
A;Accession: A32218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
R;Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Scl. U.S.A. 85, 2776-2780, 1988
A;Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi A;Reference number: A94193; MUID:88190151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Characterization of the myeloid-specific CD11b promoter. A;Reference number: 152567; MUID:92144986
A;Accession: 152567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: A46526; MUID:93123748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: granulocytes R; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G. Blood 79, 865-870, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 917-1042 <AR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: protein
Residues: 17-31 <PIE>
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Residues: 1-9 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA Residues: 1-9 <SHE>
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Ξ

Colten,

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N; Alternate names: C3 convertase; C5 convertase; complement C2
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C; Accession: A38876; B36593; I54429
R; Ishikawa, N; Nonaka, M; Wetsel, R.A.; Colten, H.R.
Submitted to GenBank, January 1991
A; Reference number: A38875
A; Accession: A38876
A; Molecule type: DNA
A; Residues: 1760 c152>
A; Coss-references: GB: M57891; GB: J05661; NID: g192436; PIDN: AAA63294.1; PID: g192437
A; Coss-references: GB: M57891; GB: J05661; NID: g192436; PIDN: AAA63294.1; PID: g192437
A; Tille: Murine complement C2 and factor B genomic and cDNA cloning reveals different
A; Reference number: A36593; MUID: 91035430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated itom upperbuyous A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule: 660-677, Mr, 679, 681-723, 'G',725 <RES> A; Cross-references: 68.M16271; NID:g199289; PIDN:AAA39562.1; PID:g199290 A; Cross-references: G8.M16271; NID:g199289; PIDN:AA39562.1; PID:g199290 C; Genetics: 16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1; 492/3; A; Introns: 16/1; 91/1; 153/1; 212/1; 224/3; 290/3; 337/1; 384/1; 414/1; 461/1; 492/3; C; Function: cleaves complement C3 and complement C5 alpha chains A; Pathway: complement C1 complement factor H repeat homology; trypsin homology; C; Superfamily: complement C2; complement factor H repeat homology (FH1) F; 22-89/Domain: complement factor H repeat homology (FH2) F; 94-149/Domain: complement factor H repeat homology (FH2) F; 94-149/Domain: complement factor H repeat homology (FH2) F; 21-60/Product: complement C2a fragment short form #status predicted (C28) F; 21-60/Product: complement C2a fragment long form #status predicted (C28) F; 21-60/Product: complement C2a fragment short form #status predicted (C28) F; 21-60/Product: complement C2a fragment short form #status predicted (C28) F; 21-60/Product: complement C2a fragment short form #status predicted (C28) F; 21-60/Product: complement C2a fragment short form #status predicted (C28) F; 21-60/Product: complement C2a fragment short form #status predicted (C28) F; 21-60/Product: complement C2a fragment short form #status F; 21-62, 49-89, 94-136, 122-149, 136-619, 136-210, 470-590, 499-515, 593-609, 647-674, 685-715/F; 21-62, 49-89, 94-136, 122-149, 136-619, 136-210, 470-590, 499-515, 593-609, 647-674, 685-715/F; 21-62, 49-89, 94-136, 122-149, 136-210, 470-590, 499-515, 593-609, 647-674, 685-715/F; 21-670, 689/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. Molecule type: mRNA
A. Residues: 1-760 < LSH>
A. Cross-references: ENBL:MS7891; NID:g192436; PIDN:AAA63294.1; PID:g192437
A. Cross-references: ENBL:MS7891; NID:g192436; PIDN:AAA63294.1; PID:g192437
A. Cross-references: ENBL:MS7891; NID:g192436; PIDN:A. Gitlin, J.; Whitehead, A.S.; C. R. Fallus, A.; Watehead, E.K.; McConnell, T.J.; Gitlin, J.; Whitehead, A.S.; C. A. Title: DNA polymorphism of MHC III genes in inbred and wild mouse strains. A. Faference number: 154429; MUID:87192938
A. Accession: 154429
A. Status: preliminary; translated from GB/EMBL/DDBJ
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24.3%; Pred. No. 0.26;
iive 38; Mismatches
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57; Conserv
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Best Local S
Matches 57
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type XII collagen alpha-1 chain - eastern newt (fragment)

C; Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C; Species: 13. Sep-1996 #sequence_revision 13. Sep-1996 #text_change 21.Jan-2000

C; Accession: 151027

K; Yang, E.V.; Yangt, K.P.; Tassava, R.A.

Dev. Biol. 168, 503.513, 1995

A; Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII (A) R; Reference number: 151027; MUID:95246925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                715 ALKFILENNF----RPGVGMREKARKIAILLTDGKSQDDIVAPSKRYA----DEGIELYAV 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMRKGIPKVLVVITDGRSQDDV----NKVSREMQLDGFSFFAIGVADADYSELVNIGSK 1077
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                                                                                                                                                                                                                                                                                        <COL1>
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 1747;
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24.2%; Pred. No. 0.2;
Live 29; Mismatches 73; Indels
                                                                               F;716-798/Domain: fibronectin type III repeat homology <FN3F>F;806-893/Domain: fibronectin type III repeat homology <FN3G> F;24-1089/Domain: von Willebrand factor type A repeat homology <F;1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>F;151-1553/Domain: non-collagenous NC2 #status predicted <NC3>F;1554-1659/Domain: triple helical domain COLI #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-929 <WEL>
                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 109.5; DE 22.9%; Pred. No. 0.41; ative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLVEKEFSAIDGVSMEPG-----
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nes 50; Conservative
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46; Conserv
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Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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C;Genetics:
A;Gene: GDB:ITGAX; CDILC
A;Gene: GDB:ITGAX; CDILC
A;Gene: GDB:ITGAX; CDILC
A;Gros-references: GDB:110758; OMIM:151510
A;Map position: 16p11.2-16p11.2
C;Superfamily: cell surface glycoprotein (DDID; von Willebrand factor type A repeat h
C;Superfamily: cell surface glycoprotein; heterodimer; magnesium; tandem repe
C;L-19/Domain: signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein (DDIC #status predicted <MAT>
F;20-1107/Domain: extracellular #status predicted <SIG>
F;20-1133/Domain: transmembrane #status predicted <TWM>
F;1108-1133/Domain: intracellular #status predicted <TWM>
F;1108-1133/Domain: intracellular #status predicted <TWM>
F;118-1163/Domain: intracellular #status predicted 
C; Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 1(XIV) chain precursor, short form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 RQGYRTAS-VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV------KDFN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 YGARRDATKILIVITDGKKEGDSLDYKD-VIPWADAAGIIRYAIGVGLAFQNRNSWKELN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 ETQLARIAD--SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 9.1%; Score 103; DB 1; Length 1163; Best Local Similarity 24.5%; Pred. No. 0.91; Matches 45; Conservative 33; Mismatches 72; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S31212

K;Waelchi, C; Trueb, J; Kessler, B.; Winterhalter, K.H.; Trueb

Bur. J. Biochem. 212, 483-490, 1993

A;Title: Complete primary structure of chicken collagen XIV.

A;Reference number: S31211; MUID:93185668

A;Accession: S31212

A;Status: nucleic acid sequence not shown; translation not shown
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                A.Status: preliminary
A.Molecule type: nucleic acid
A.Molecule type: nucleic acid
A.Molecule type: nucleic acid
A.Molecule type: nucleic acid
A.Molecule type: nucleic acid
A.Molecule type: nucleic acid
A.Molecule type: nucleic acid
A.Mote: Sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
C.Superfamily: thrombospondin type I repeat homology; von Willebrand factor type A repeat homology cTHR2>
F.45-218/Domain: von Willebrand factor type A repeat homology cTHR2>
F.32-296/Domain: thrombospondin type I repeat homology cTHR2>
F.317-413/Domain: thrombospondin type I repeat homology cTHR4>
F.43-433/Domain: thrombospondin type I repeat homology cTHR4>
F.444-556/Domain: thrombospondin type I repeat homology cTHR5>
F.50-610/Domain: thrombospondin type I repeat homology cTHR6>
                                                                                                                               R; Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Blochem. Parasitol. 57, 171-174, 1993
A;Title: Sequence of a major Elmeria maxima antigen homologous to the Eimeria tenella mi
A;Reference number: A48569; MUID:93149203
A;Accession: A48569
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Note: this revision to the sequence from reference A35543 includes the carboxyl end
R; Corbi, A L.; Garcia-Aguilar, J.; Springer, T.A.
B; Biol. Chem. 255, 2788, 1990
A; Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A; Reference number: A35543; MUID:90153906
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A;Reference number: S00864; MUID:88166645
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A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence.revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A36584, A35543; S00864
R;Corbi, A.L.; Garcia-Aquilar, J.; Springer, T.A.
J; Bill. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
                              .Species: Eimeria maxima
.Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: this sequence has been revised in reference A36584
R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 ARIA--DSKDHV-FP--VNDGFQALQGIIHSILKKSCIEI----LAAEPSTI--CAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
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Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.3%;
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Best Local Similarity 27.0'
Matches 48; Conservative
   antigen Em100 - Elmeria maxima
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C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C; Accession: A37979; B37979
R; Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.;
J; Biol. Chem. 265, 19624-19631, 1990
A; Title: Structure and chromosomal location of the human gene encoding cartilage matr
A; Reference number: A37979; MUID:91060568
                                                                                                                                                                                                                    c;Superfamily: unassigned EGF-related proteins; EGF homology; von Willebrand factor C;Reywords: glycoprotein; homotrimer F;1-22/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;MOJECULE type: mRNA
A;Residues: 157-290, L', 292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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A;Experimental source: Clostridium acetobutylicum ATCC824
1194 PSERHVFFVDD-FDAFTKIEDELITFVCETASATCPLVFKDGDKLA-----GFKMMEMF 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RTASVIIALTDGELHEDLFFYSER----EANRSRDLGAIVYCVGVKDFNETQLARIADSK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605 GDCEVVV-LIDGQ-----WYGKKDIMAEVNKCKEYEIBIAAIGFGNAKKDFLDKIATCE 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSFIVESTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550 LALIGFADKVKTLINLTEDREEIFRAIDGEKKADVGTST-MSEPFSEA----YNILKDAY
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                                                                                                             1271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.8%; Score 99; DB:
27.0%; Pred. No. 1.1;
tive 28; Mismatches
                                                           174 DRVLCSFKINDSVTLSKSLQSPWVSSTSGFKEGNSHPC
                                                                                                               -TFNVYPC
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A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1;
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:127280; OMIM:115437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage matrix protein precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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A;Accession: B37979
                                                                                                                  1247 GLVEKEFSAIDGVSMEPG-
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A; Molecule type: DNA
A; Residues: 1-496 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-698 <KUR>
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EN 659
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Best Local Sim:
Matches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
A; Gene: CAC0473
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1868 < TRU:
A; Residues: 1-1868 < TRU:
A; Trueb, J: Kessler, B.; Winterhalter, K.H.; Trueb, B.
B; Cross-references: EMBL: X70793; NID:9288872; PIDN:CAA50064.1; PID:9288873
A; Title: Complete primary structure of chicken collagen XIV.
A; Reference number: S1211; MUID:9318568
A; Accession: S31211
A; Stetus: preliminary
A; Molecule type: mRNA
A; Residues: 1-416;1460-1811,1843-1888 < WAE>
A; Molecule type: mRNA
A; Residues: 1-416;1460-1811,1843-1888 < WAE>
A; Molecule type: mRNA
A; Residues: 1-416;1460-1811,1843-1888 < WAE>
A; Cross-references: EMBL: X70793
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: colladen alpha 1(XIV) chain; fibronectin type III repeat homology < FN3A>
F; 29-180 Product: collagen alpha 1(XIV) chain; long form #status predicted < MAT>
F; 29-180 Product: collagen alpha 1(XIV) chain; long form #status predicted < MAT>
F; 29-110/Domain: signal sequence #status predicted < MAT>
F; 29-110/Domain: fibronectin type III repeat homology < FN3B>
F; 320 / Momain: fibronectin type III repeat homology < FN3B>
F; 3442-525 / Domain: fibronectin type III repeat homology < FN3B>
F; 3442-525 / Domain: fibronectin type III repeat homology < FN3B>
F; 3442-525 / Domain: fibronectin type III repeat homology < FN3B>
F; 3442-525 / Domain: fibronectin type III repeat homology < FN3B>
F; 3442-525 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Domain: fibronectin type III repeat homology < FN3B>
F; 320-1009 / Do
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen alpha 1(XIV) chain precursor, long form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
C;Accession: S78476; S31211
R;Irueb, B.
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                                                                                                                                                                                                                                                                                                                                       1194 PSERHVFFVDD-FDAFTKIEDELITFVCETASATCPLVFKDGDKLA-----GFKNMEMF 1246
                                                                                                                             1082 VAIIQFSDDPRTEFKLNAYKTKTTLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEA 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSFIVESTRGTTLMKLT--EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                           115 -SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV 173
                                                                                                                                                                                      GYRTA--SVIIALTDGELHEDLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD- 114
                                        Gaps
                                                                                                                                                                                                                          MSFIVESTRGTTLMKLT - - EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQ
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                                        35;
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                                        Indels
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                                        98;
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                                                                                                                                                                                                                                                                                                                                                                                                   174 DRVLCSFKINDSVTLSKSLQSPWVSSTSGFKEGNSHPC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 102.5; I 22.5%; Pred. No. 1.9; tive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, January 1993
A;Reference number: S78476
A;Accession: S78476
                                           Mismatches
                                              36;
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Best Local Similarity 22.5%
Matches 49; Conservative
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                                                 Conservative
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                                                   Matches
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A. Moclecule type: protein; mRNA
A. Moclecule type: protein; mRNA
A. Moclecule type: protein; mRNA
A. Moclecule type: protein; mRNA
A. Moclecule caid translation differs from the sequence shown in having 300-Leu, 3
A. Mote: 736-Sex as a sloo found
A. Mote: 919-Cosylation sites were determined
A. Mote: 919-Cosylation sites
A. Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of
A. Contents: the final paper in a series documenting the sequence, glycosylation site,
A. Moclecule type: protein
A. Reference number: A19188: WUID: 83204002
A. Moclecule type: Drotein
A. Reference number: A19947; WUID: 83273641
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: MNA
A. Molecule type: MNA
A. Molecule type: DNA
A. Molecule type: MNA
A. Molecule type: MNA
A. Molecule type: DNA
A. Molecule type: MNA
A. Molecule type: DNA
A. Molecule type: MNA
A. MOLecule ty
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A; Residues: 467-546; 550-595; 752-764 <MOO>
A; Cross-references: GB:J00185; GB:J00186
A; Note: the authors translated the codon TAC at 519 as Thr; the nucleic acid translat
A; Mole, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
A; Mole, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
A; Title: Complete primary structure for the zymogen of human complement factor B.
A; Reference number: A20751; MUID:84161997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Internal homologies of the Ba fragment from human complement component facto A,Reference number: A44628; MUID:84158524
                                                                                                                                                                                                                                                                                                                                                                                                         a class
C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000 C;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339; A44628; R;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G. Aille, Committed to the EMBL Data Library, March 1993 A;Reference number: S34075 A;Reference number: S34075 A;Accession: S34075
                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-764 <MEJ>
A; Cross-references: EMBL:X72875; NID:g297568; PIDN:CAA51389.1; PID:g297569
A; Cross-references: EMBL:X72875; NID:g297568; DIDN:CAA51389.1; PID:g297569
R; Woods, D. E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A; Title: Isolation of cDNA clones for the human complement protein factor B,
A; Reference number: A44622; MUID:83039428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A;Residues: 270-329 <NIE>
A;Note: binding site for carbohydrate to lysine under artificial conditions
E;Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
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A;Molecule type: mRNA
A;Residues: 16-225,'F',227-259 <MOR>
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A; Residues: 1-99 <WUL>
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N.Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-
N.Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinesin-like protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50240
R;Cadieu, E.; Lelaure, V.; Galibert, F.; McDougall, R.C.; Rajandream, M.A.; Barrell, S. Submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: Z25048
A;Scacssion: T50240
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-817 <CAD>
A;Cxoss-references: EMBL:AL136235; PIDN:CAB65811.1; GSPDB:GN00066; SPDB:SPAC664.10
A;Experimental source: strain 972h(-); cosmid c664
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGAIVYCVGVKDFNETQLARIADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEP 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       39 TYMHEGFERASEQIY----YENRQGYRTAS--VIIALTDGELHEDLFFYSEREANRSRD 91
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F;39-206/Domain: von Willebrand factor type A repeat homology <WWAl>
F;227-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology <WWA2>
F;273-437/Domain: von Willebrand factor type A repeat homology <WWA2>
F;76,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;221-238,234-247,249-262/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                 DB 2;
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29.7%; Pred. No. 1.2;
tive 19; Mismatches
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Pred. No. 2.
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25.1%;
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity 29.79
Matches 41; Conservative
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A;Map position: 1
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                                                                                                                                                                                                                                                                                                 Query Match
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STICAGES --- FQVVVRG 164
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Best Local Similarity 29.09
Matches 40; Conservative
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Job time: 262 sec
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A;Gross-references: GDB:119726; OMIM:138470
A;Hap position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; 69
A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor
ment factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                   A;Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conv A;Reference number: 157824; MUID:94067177
A;Accession: 157824
  zum Busche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alpha
                       Title: Human complement factor B: functional properties of a recombinant zymogen of Reference number: 154409; MUID:94041399
                                                                                                                                                     A;Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.
Mol. Immunol. 30, 1387-1592, 1993
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        E.H.; Meyer
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-31, '0', 33-764 <RE2>
A;Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922
C;Comment: 292-Cys has a free sulfhydryl.
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R;Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties of a rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.4%; Score 95; DB 1; Length 764; 20.3%; Pred. No. 2.7; sive 32; Mismatches 69; Indels
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                                                                                       A; Accession: 154409
A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                      Molecule type: mRNA
Residues: 1-764 <RES>
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Matches 45
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A;Gene: GDB:BF
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S66522 cartilage matrix protein precursor - mouse

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S66522.
R;Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein A;Reference number: S66522; MUID:96270751
A;Accession: S66522
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A; Residues: 1-500 <ASZ>
A;Cross.references: EMBL:U35035; NID:91163178; PIDN:AAB06521.1; PID:91163179
C;Genetics:
Species: Mus musculus (house mouse)
Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
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29.0%; Pred. No. 2.1;
tive 20; Mismatches
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A human TANGO 216
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Human novel extrac
Amino acid sequenc
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203.258 Million cell updates/sec
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1 MSFIVFSTRGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                              747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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AAE01469
                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                     Human protein sequence SEQ ID NO:11706
         AAB92985 standard; Protein; 218 AA
                                                                                                                                                                                             29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-RAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-02418999.
                                                                                                                                                                           28-JUL-2000; 2000EP-0116126
                                                  (first entry)
                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34
                                                                                                               Homo sapiens
                                                                                                                                   EP1074617-A2
                                                  26-JUN-2001
                                                                                                                                                       07-FEB-2001
                                                                                                                                                                                                                                                                                          Ishii S,
                              AAB92985;
AAB92985
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Primer sets for synthesizing polynucleotides, particularly the 5602

26-JUL-2001

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121 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                               RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                       full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                              .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                             181 KINDSVILSKSLOSPWVSSTSGFKEGNSHPCLPARPHT 218
                                  2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM38976 standard; Protein; 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                        of the present invention.
                                      Claim 8; SEQ ID 11706;
                       full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia
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WO200153312-A1

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostation containing a polypeptide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide of of the invention may be used to treat diseases of the peripheral nervous contains and neuropathy and central nervous system diseases, such as localised neuropathies and central nervous system diseases, and stripping a local stripping and syndrome. Other uses include the attain activity, nemotatic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and contain and activity arthritis and inflammation, leukaemias and activity and processes.
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                                                                                                                                                                                                                                                                                                              useful for treating disorders
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Yang Y,
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100.0%; Pred. No. 5e-124;
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0; Mismatches 0;
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 2121; 10078pp; English.
                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, us
such as central nervous system injuries
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                                                            2000US-05817.
2000US-052317.
2000US-059042.
2000US-062312.
200US-0653450.
2000US-0653450.
2000US-0633036.
                                 26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 218; Conservative
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Wang Z, V
Zhou P,
                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                        03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
29-NOV-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, poscriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chisease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial C TANGO-128, 140, 197, 213, 214, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, prognostic assays, paramacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a clisorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
                                                                                                TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; Septic Shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 pvndgfqalqqilhsilkkscieilaaepsticagesfqvvrgngfrharnvdrvlcsf 259
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Pred. No. 1.5e-104;
2; Mismatches 0;
                                                                                                                                                                                                                                 prognosis; prophylatic; therapeutic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Fig 4; 209pp; English.
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98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                              98US-0223546.
                                                                                                                                                                                                                                                                                                                                                                        99WO-US31025
                               20-OCT-2000 (first entry)
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es 188; Conserv
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                                                                    Human TANGO 197.
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                                                                                                                                                                                                                                                                    Homo sapiens.
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AAB01422;
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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted protein or gene therapy. Pathological conditions can be diagnosed by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the control of the developing products for the diagnosis or treatment of proliferative disorders, cancer, thumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AlDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; sdisease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
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30-JUN-2000; 2000US-0215133.
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skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound classorders, and infections. The proteins can also be used to aid wound calling and epithelial cell proliferation, to prevent skin aging due to submurn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their compate ligands or binding partners, and in chemotaxis, and can be used in a set food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunossays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                  Score 966; DB 22; Length 403; Pred. No. 2e-104;
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                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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/note= "Encoded by GKT"
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28..403
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98.9%;
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Best Local Similarity
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AAD05300-AAD05379 represent CDNAs corresponding to 28 human secreted protein genes, and AAE01446-AAE01513 represent the proteins they encode. CC AAE01544 represent human secreted protein fragments or variants. CAAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, creating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the cannot of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new genes. Specific uses are described for each of the immunity of the interpretative disorders, cancer, tumours, foetal and developmental products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental continued disorders, diseases of the immune system, allerative disorders, conditive disorders, schizophrenia, asthma, callerative disorders, conditive disorders, schizophrenia, asthma, cardiovascular disorders, pregnancy-related disorders, earlierative disorders, pregnancy-related disorders, endicated disorders, maninear disorders, pregnancy-related disorders, endicated disorders, and infections. The proteins can also be used to aid wound disorders, and infections. The proteins can also be used to aid wound conture of primary tissues, to regenerate tissues, to identify their culture of primary tissues, to regenerate tissues, to identify their culture of primary tissues, to regenerate tissues, and can be used on a a food additive or preservative to modify storage properties.

Calleviating symptoms associated with the disorders mentioned above, and immunosorbent assay (ELISA). The present sequence represents a human immunosorbent assay (ELISA). The present sequence represents a human immunosorbent assay (ELISA). The present sequence represents a human immunosorbent assay (ELISA).
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Pred. No. 7.9e-104;
2; Mismatches 1;
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"Encoded }
                /label- Unknown
/note= "Encoded
Misc-difference 368
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ilarity 98.4%;
Conservative
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30-JUN-2000; 2000US-0215133.
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/note=
Misc-difference 331
                                                                                                                    /note=
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Best Local Simi
Matches 187;
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                                                                                                                                                                                                                                                                                    cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchicatis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                     140 rtasviialtdgelhedlffysereanrsrdlgaixycvgvkdfnetglariadskdhvf 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44..213
/40.e= "von Willebrand factor A domain"
                                                                                                                                                                                                                                                                          TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                                               Amino acid sequence of human TANGO 216 polypeptide.
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hte= "transnmembrane domain"
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98..317
//orte= "cytoplasmic domain"
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/note= "mature protein"
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                                                                                                                                                                    AAB18447 standard; Protein; 488 AA.
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342..488
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/note=
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260 kindsvtlne 269
                                                                          KINDSVTLSK 190
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Peptide
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The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. THE TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any won Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular interactions, modulate cell adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, differentiation, differentiation, differentiation, differentiation, differentiation, differentiation, differentiation and bronchies, solen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disorders, treat cardiovascular disorders such as ischemic heart disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the covaries, cerebral ocedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, becterial and viral meningitis, latrogenic disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, disorders, hydrocephalus and encephalitis, and treat hepatic
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53.4%; Pred. No. 3.3e-50;
ive 37; Mismatches 49;
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Matches 101; Conservative
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258 tynetytts 266
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15-JAN-2001 (first entry)

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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC CO describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC pollypeptides can be used to medulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The cord of disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, compute cell adhesion in proliferative disorders, such as cancer, and the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, and hematopoietic associated diseases and disorders, spheen associated accent and hematopoietic associated diseases and disorders, spheen associated diseases, modulate renal disorders, treat cardiovascular disorders associated diseases, modulate renal disorders, treat cardiovascular disease, modulate renal disorders, and cerebral oedema, hydrocephalus, brain herniations, introgenic disease, inflammations, cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to treat disorders associated disease, introgenic disease, inflammations, brain menigitis, alzheimer's Disease, crebral carecrs, toxocophalus, brain menigitis, alzheimer's Disease, crebral carecrs, receptance disease, intrammations, introgenic disease, inflammations, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.

Created using information provided.
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;; Pred. No. 3.3e-50;
37; Mismatches 49;
                                                                                                                                                Fraser CC;
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cal Similarity 53.4%;
101; Conservative 37
                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                       01-MAR-2000; 2000WO-US05226.
                                                                          99US-0122458.
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258 tvnetytts
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO CC describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO CC polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, and cell trafficking and/or migration, modulate cellular interactions, cc modulate the proliferation, differentiation, and/or function of cells cand hematopoletic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial sthma and bronchiectasis, intestinal disorders, splean associated asthma and bronchiectasis, intestinal disorders, splean associated as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, iatrogenic disease, inflammations, iatrogenic disease, inflammations, hydrocephalus and encephalitis, and treat hepatic disorders.

Croxoplasmosls, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders:

Croxoplasmosls, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders:

Creat disorders associated with the specification; it was note: the present sequence does not appear in the specification; it was one created using information provided.
                                                                                  TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                       A human TANGO 216 polypeptide clone.
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Best Local Similarity 53.4%;
Matches 101; Conservative 3
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181 KINDSVTLS 189
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258 tynetytts 266
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24 - FEB - 2000;
02 - MAR - 2000;
17 - MAR - 2000;
18 - APR - 2000;
19 - MAY - 2000;
07 - JUN - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANGO 266; TANGO 216;; TANGO 261; TANGO 267;

cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoletic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                      80 lsfivfssgatiilpltgdrgkiskgledlkrvspvgetyiheglklanegi--gkaggl 137
                                                             61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                        Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                              PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18457 standard; Protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2000; 2000WO-US05226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0122458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-579269/54.
N-PSDB; AAA75159.
                                                                                                                                                                                                                                                                                            KINDSVTLS 189
                                                                                                                                                                                                                                                                                                                                                      tynetytts 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18457;
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AAB18457
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as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage earlis and to treat bone and/or treat disorders associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

once: the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; inrombolytic; antimicrobial; ophthalmic; oytostatic; antialzheimers; immuno-dautoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinso's sisease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.7%; Score 506; DB 21; Length 488; 53.4%; Pred. No. 3.3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human novel extracellular matrix protein, Seq ID No 312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.3e-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU19662 standard; Protein; 587 AA.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.4%;
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2000US-0184664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0186350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 53.4 Matches 101; Conservative
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PR 28-JUN-2000; 2000US-021586.
PR 70-JUN-2000; 2000US-0215815.
PR 70-JUN-2000; 2000US-0215880.
PR 70-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0216890.
PR 14-JUL-2000; 2000US-022056.
PR 14-AUG-2000; 2000US-0225214.
PR 12-AUG-2000; 2000US-0225214.
PR 12-AUG-2000; 2000US-0225214.
PR 12-AUG-2000; 2000US-022314.
PR 12-AUG-2000; 2000US-022314.
PR 12-AUG-2000; 2000US-022314.
PR 12-AUG-2000; 2000US-022314.
PR 12-SEP-2000; 2000US-022314.
PR 12-SEP-2000; 2000US-023124.
PR 14-SEP-2000; 2000US-023134.
PR 14-
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PR 20-CCT-2000 200008-024186.

PR 20-CCT-2000 200008-024186.

PR 20-CCT-2000 200008-024186.

PR 20-CCT-2000 200008-024186.

PR 20-CCT-2000 200008-024186.

PR 08-WY-2000 200008-024471.

PR 08-WY-2000 200008-024471.

PR 08-WY-2000 200008-024471.

PR 08-WY-2000 200008-024457.

PR 08-WY-2000 200008-024457.

PR 08-WY-2000 200008-024452.

PR 08-WY-2000 200008-024552.

PR 17-WY-2000 200008-02452.

PR 17-WY-2000 20008-02452.

PR 17-WY-2000 20008-02452
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e.g.

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be administered to treat diseases by gene therapy. Antisense molecules may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of antagonists may also be used to down regulate expression and activity of SPs and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) neurological diseases (e.g. Alzheimer's disease, arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and coular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hematopoietic associated disease; atelectasis; pulmonary congestion; ocedema: emphysema; chronic bronchital asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; renal disorder; schemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
expression of SPs. The SP polynucleotide or a vector expressing them may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETOLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 505; DB 22;
Pred. No. 5.8e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 5.8e 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB18448 standard; Protein; 487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          53.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 53.49
Matches 101; Conservative
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80..97
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
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disorders, atclectasis, pulmonary congestion or oedema, emphysema chronic bronchitis, bronchial asthma and bronchicetasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, crebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a murine TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO DOLYPEPLIDES can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                    Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
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                                                                                                                                                                                                                                                                                              Fraser CC;
                                  "transnmembrane domain"
                                                                       "extracellular domain"
"cytoplasmic domain"
                                                                                                                                                                                                                                                                                              Sharp JD,
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                                                                                                                                                                                                                                                       MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                  01-MAR-2000; 2000WO-US05226.
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Matches 102; Conservative
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Length 487;

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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 264, TANGO 262, and TANGO 267. The TANGO CG describes TANGO 266, TANGO 267, TANGO 267, TANGO 267. The TANGO CC describes TANGO 266, TANGO 267, TANGO 267. The TANGO CC polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or music cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, requilate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, condulate the proliferation will ferentiation, and/or function of cells and hematopoietic associated diseases and disorders, atelectasis, can hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, integrinal disorders, spleen associated disease, modulate renal disorders, treat cardiovascular disorders such associated diseases, modulate renal disorders, treat cardiovascular disorders associated disease, or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, lattogenic disease, inflammations, corpusamosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. They was concerted using information provided.

C created using information provided.
                                                                                                                                                                                               rango 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedems; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; menhigitis; Alzhenner's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sharp JD, Fraser CC;
                                                                                                                                                                   A murine TANGO 216 polypeptide clone.
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                                    AAB18458 standard; Protein; 487 AA.
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                                                                                                                                   61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                     121 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                      Gaps
                                                              1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
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                                 Indels
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43.8%; Score 495; DB 21;
53.7%; Pred. No. 6.5e-49;
                A murine TANGO 216 polypeptide clone.
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(MILL-) MILLENNIUM PHARM INC.

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modulate cell adhesion in proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, plood and hematopoietic associated diseases and disorders, atelectasis, blood asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as Ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral cedema, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzhainer's Disease, inflammations, bacterial and viral meningitis, and treat hepatic disorders.

Copplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Coreated using information provided.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     43.8%; Score 495; DB 21; Length 487; 53.7%; Pred. No. 6.5e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Mismatches
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Matches 102; Conservative
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258 tanstytkse 267
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO CO OC describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO CO OLYPEPtides can be used to omodulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, and cell trafficking and/or migration, modulate cellular interactions, compulate the proliferation differentiation, and/or function of cells can hematopoiette associated diseases and disorders, atelectasis, blood and hematopoiette associated diseases and disorders, spleen associated diseases, modulate trenal disorders, spleen associated diseases, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart diseases or disorder. They may also be used to treat disorders associated with the ovaries, and crebral one and/or cartilage associated with the ovaries, and crebral one and/or treat disorders associated with the ovaries, and crebral one companion, bacterial and viral meningitis, Albahaer's Disease, cerebral cancers, hydrocephalus, brain henniations, is atrogenic disease, inflammations, hydrocephalus, brain modulate, multiple sclerosis, brain cancers, hydrocephalus, and ercephalus, and treat hepatic disorders, it was not encephalus, and treat hepatic disorders, created using information provided.
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                                                                                                                                          Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
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                                       Fraser CC;
                                       Sharp JD,
                                                                                                                                                                                                                             Disclosure; Page -; 175pp; English.
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Matches 102; Conservative
                                                                                                                                                                  262, 266 and 267 useful a e.g. for treating cancer
                                         DA,
                                         Holtzman
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258 tanstytkse 267
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N-PSDB; AAA75162.
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases e.g. mysthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial cansoric biology, for diagnostic assays, prognostic assays, forensic biology, for diagnostic assays, prognostic assays, paramacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 27; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                    98US-0223546.
                                                                                                                                                                                                                                                                                            99WO-US31025
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-465743/40.
N-PSDB; AAA47479.
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                                                                                                                                                                          Mus musculus.
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ó 108 QLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 167 Gaps ;; 0 Score 415; DB 21; Length 381; Pred. No. 1.1e-39; Indels .; 0 2; Mismatches 36.7%; 97.6%; Conservative Query Match Best Local Similarity 81; Best_Loca Matches ŏ g

168 RHARNVDRVLCSFKINDSVTLSK 190

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Search completed: August 9, 2002, 10:32:15 Job time: 134 sec

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Sequence 55, Appl
Sequence 2, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 2, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 69, Appl
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Sequence 3, Appli
                                                                                                                                                                                                                                                                                     APPLICANT: Gallatin, W. Mich
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TTILE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTYRY: United States
ZIP: 60606-640.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPASSIONS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
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Best Local Similarity 28.2%; Pred. No. 1.9e-09;
Matches 66; Conservative 42; Mismatches 96
     US-08 605-672-55
US-08 462-293A-2
US-08 482-293A-29
US-08 482-293A-99
US-08 943-363-2
US-08 943-363-2
US-08-193-043-2
US-09-193-043-2
US-09-193-043-99
PCT-US95-04439-1
US-08-4-6062A-43
5424399-2
                                                                                                                                                               US-08-173-497-3
US-08-286-889-3
                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
TELEPRAX: 312-474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                         Sequence 46, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1155 amino acids
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1161
1161
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11153
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MOLECULE TYPE: protein
US-08-286-889-46
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 FILING DATE:
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US-08-286-889-46
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1114400
114450
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178.842 Million cell updates/sec
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1 MATAERRALGIGFQWLSLAT......TTHCSLHKIASGPTTAACME 333
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Sequence 46,
Sequence 46,
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Sequence 53,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/pcvuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcvuS_COMB.pep:*
                    Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
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US-08-362-652-55
         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB
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LTEDR-----EQIROGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                      95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                   149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                              144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit

TITLE OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, V. Toole, Gerstein, Murray & Borun

ADDRESSEE: Marshall, N. Dole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                 Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606-6402
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%; Score 166; DB 1;
28.2%; Pred. No. 1.9e-09;
Live 42; Mismatches 96
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CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-MG-1994
ATTONNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/COCKET NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        ; Sequence 46, Application US/08362652
; Patent No. 5766850
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TELEX: 25-3856
INFORMATION FOR SEO ID NO: 46:
SEQUENCE CHARACTERISTICS:
SEQUENCE TARGET SEO ID NO: 46:
SEQUENCE TARGET SEO ID NO: 46:
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COUNTRY: United States
ZIP: 60606-6402
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                                                                                                              149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                          95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                  200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                            9.6%; Score 166; DB 1; Length 1155; 28.2%; Pred. No. 1.9e-09; Live 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Marshall, O'Toole, Gerstein, Murray
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46, Application US/08485618
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 572853361 Human 2
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27866/32797
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APPLICATION WOMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION UNDRER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/362,652
FILING DATE: 21-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACIERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.23
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-485-618-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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US-08-485-618-46
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                    Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                      200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                   | : | | | : | | | : | | | | : | | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 166; DB 2; Length 1155;
28.2%; Pred. No. 1.9e-09;
Live 42; Mismatches 96; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chlcay-
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~MPUTER: IBM PC COMPATIBLE
~~MPUTER: IBM PC COMPATIBLE
~~MPUTER: IBM PC COMPATIBLE
~~MPUTER: IBM PC COMPATIBLE
~~MPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
FELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.2%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                RESULT 5
US-08-482-293A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-482-293A-46
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204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                 149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                          144 PECPGOEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                              200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                          | : | ||: | | : | | : | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.6%; Score 166; DB 2; Length 1155; 28.2%; Pred. No. 1.9e-09; tive 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECHONINICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                                                                                                                                                                                                                       US-08-605-672-46
; Sequence 46, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRP PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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Best Local Similarity
Matches 66; Conserva
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149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 PACYG-GEDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
AITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                                                 Score 166; DB 4; Length 1155; Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITIE OF INVENTION: No. 6251395el Human 2
FILE REPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER PILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER: OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF COUNTY OF 
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Patent No. 5728533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/09193043
Patent No. 6251395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 28.2
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                 Sequence 46, Application US/08943363
Sequence 46, Application US/08943363
Sequence 46, Mplication US/08943363
GENERAL INFORMATION:
GAPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                          316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STRME: 11linois COUNTRY: United States
ZIP: 60606-6402
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: 1BM PC Compatible COMPUTER: 1BM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILLING DATE:
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28.2%; Pred. No. 1.9e-09;
Live 42; Mismatches 96; Indels 3
                                                    TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION UNBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORING DATE: 1-DEC-1994
ATTORING NAME: APPLICATION NUMBER: US 08/362,652
FILING DATE: 1-DEC-1994
ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORING NAME: ATTORI
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TELEPHONE: 312-474-6300
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LENGTH: 1155 amino acids
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Best Local Similarity 28.2%
Matches 66; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312-474-0448
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144 PECPGGEMDIAFLIDGSGSIDGSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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Batent No. 5817515

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTON: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%; Score 166; DB 1;
28.2%; Pred. No. 1.9e-09;
tive 42; Mismatches 96
                                                                                                                                                     FILING DATE:
CLASSIFICATION (435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTONNEY,AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
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REFERENCE/DOCKET NUMBER: 38,659
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE#1.0, v
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INFORMATION FOR SEQ ID NO: 53
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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312-474-0448
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Best Local Similarity 28.2%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-362-652-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-605-672-53
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Sequence 53, Application US/08362652

Sequence 53, Application US/08362652

Patent No. 5766650

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
NUMBER OF SEQUENCE: 93

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.6%; Score 166; DB 1; Length 1161; 28.2%; Pred. No. 1.9e-09;
                                                                                                   SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/485,618 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Mismatches
                                                                                                                                                                                                                                                        PELICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 5-AUG-1994
PROR APPLICATION NUMBER: US 08/362,652
FILING DATE: 1-DEC-1994
PROR APPLICATION DATA: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRN: 312-474-6300
TELEFRX: 312-474-6300
TELEFRX: 312-474-6300
SEQUENCE CHARACTERISTICS:
                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1161 amino acids
                                 Floppy disk
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-485-618-53
                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53, Application US/08943363
Sequence 53, Application US/08943363
Sequence 53, Application US/08943363
Sequence 54, Application US/08943363
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
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9.6%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 1.9e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 34
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                             FILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 3.0EC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5.04G-1994
FILING DATE: 2.056-1994
FILING DATE: 2.056-1994
APPLICATION NUMBER: US 08/362,652
FILING DATE: 2.056-1994
APPLICATION NUMBER: 30.659
REGISTATION NUMBER: 38,659
REGISTATION NUMBER: 38,659
REGISTATION NUMBER: 38,659
REGISTATION NUMBER: 32,636
TELEFAX: 312-474-046
TELEFAX: 312-474-046
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 and acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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APPLICATION NUMBER: US/08/482,293A
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-482-293A-53
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US-08-943-363-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.6%; Score 166; DB 2;
Best Local Similarity 28.2%; Pred. No. 1.9e-09;
Matches 66; Conservative 42; Mismatches 96
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GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5831029el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                       PELLIN DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-A0G-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: WALLIAMS J. JOSEPH
REFERENCE/DOCKET NUMBER: 38-659
RECISTRATION NUMBER: 38-659
REFERENCE/DOCKET NUMBER: 37866/32684
TELECHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                               27866/32684
                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53, Application US/08482293A Patent No. 5831029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-605-672-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-482-293A-53
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                                                                                                                                                                                                                                                                                                      204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                               149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                       259 TOGOKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
                                                                                                                                                                                                         95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                             37 PACYG-GEDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: | ||: | ||: | | :| | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
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                                                                                       Length 1161;
                                                                                                                                  96; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.2%; Score 159.5; DB 1;
27.9%; Pred. No. 1e-08;
tive 41; Mismatches 93;
                                                                                     Query Match 9.6%; Score 166; DB 4; Best Local Similarity 28.2%; Pred. No. 1.9e-09; Matches 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRYS: 312-474-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
STATE: United States
ZUD: 60606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37:
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LENGTH: 1151 amino acids
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Best Local Similarity 27.94
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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; ORGANISM: Mus musculus US-09-193-043-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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STREET: 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.6%; Score 166; DB 2; Length 1161;
28.2%; Pred. No. 1.9e-09;
tive 42; Mismatches 96; Indels 3
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APPLICAMT: Van der Vieren, Monica
TITLE DE INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER PELING DATE: 1993-12-23
EARLIER PELING DATE: 1994-08-05
EARLIER PELING DATE: 1994-08-05
EARLIER PELING DATE: 1994-12-21
EARLIER PELING DATE: 1994-10-03
EARLIER PELING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. RECISTRATION NUMBER: 38,659
REFENCE/DOCKET NUMBER: 27866/32684
TELECOMMINICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 53, Application US/09193043 Patent No. 6251395 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 66; Conserv
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SEQ ID NO 53
LENGTH: 1161
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US-09-193-043-53
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US-08-485-618-37
US-08-485-618-37
Sequence 37. Application US/08485618
Sequence 37. Application US/08485618
Sequence 37. Application
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
TITLE OF INVENTION: 103
CORRESPONDENCES: 103
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                    98 DREGIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 156
                                                       DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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9.2%; Score 159.5; DB 1;
Best Local Similarity 27.9%; Pred. No. 1e-08;
Matches 63; Conservative 41; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-0448
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,656,652
REGISTRATION NUMBER: 38,656,652
REGISTRATION NUMBER: 38,656,652
REGISTRATION NUMBER: 38,656,652
REGISTRATION NUMBER: 38,656,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 233 SOUTH Wacker Drive, 65 CITY: Chicago STATE: Illinois COUNTY: United States ZIP: 6666-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COM
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 1151 amino acids amino acid
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98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 156
                                                157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 207
                                                                                    97
44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                               LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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Search completed: August 9, 2002, 10:33:10 Job time: 189 sec

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; Search time 102.68 Seconds
(without alignments)
561.037 Million cell updates/sec
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1 MATAERRALGIGFOWLSLAT......TTHCSLHKIASGPTTAACME 333
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sp_phage:*
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2: sp_bacteria:*
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4: sp_human:*
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Sequence:
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                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ption	296p02 homo sapien	homo sapien	296ec6 homo sapien	Q9qye7 rattus norv	halocynthia	Q04588 eimeria max	eimeria ten	070350 mus musculu	neospora ca	homo sapien	homo sapien	sus scrofa	caenorhabdí	O rattus norv	099117 mus musculu	7 mus musculu
		Description	036p02	096nc7	096ec6	09qye	Q9bpq8	004588	043981	07035	09u8j9	043853 1	O9ugc3	028984	Q9ua13	09113	11660	09es77
SUMMARIES		ID	Q96P02	Q96NC7	Q96EC6	Q9QYE7	Q9BPQ8	004588	043981	070350	608060	043853	Q9UGC3	Q28984	Q9UA13	097130	Q99L17	Q9ES77
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		Query Match Length DB	368	245	97	1161	1332	724	712	160	765	517	099	920	3767	1151	221	3567
	æ	Query Match	95.4	33.7	27.0	9.5	8.9	8.7	8.0	7.8	7.7	7.6	7.6	7.6	7.4	7.1	7.0	6.9
		Score	1649	582	467	159.5	153.5	150.5	137.5	134	132.5	131.5	131	130.5	128	123	121	118.5
	;	Result No.	П	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16

181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240

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Q99218 homo sapien O53870 mus musculu Q21281 caenorhabd1 Q96414 caenorhabd1 Q96415 homo sapien O00261 homo sapien O95721 mus musculu Q9xtp6 plasmodium Q9yic5 cyprinus ca Q9ff49 arabidopsis O97566 canis famil Q99k64 mus musculu Q01510 plasmodium Q91900 xenopus lae Q923x3 mus musculu Q18048 caenorhabdi O00816 toxoplasma Q94xh4 mus musculu Q63001 rattus norv Q6400 rattus norv Q6600 rattus capien Q94674 plasmodium Q948g7 oryza sativ Q660 rattus caenorhabdi Q01506 plasmodium Q01508 plasmodium	AA. upda on up erteb Homi 11er for A	ACY ACY ACY ACY ACY ACY ACY ACY ACY ACY
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Rattus norvegicus
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SEQUENCE FROM N.A.

Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Ninomiya K., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Furuya T., Takahashi M., Tanikawa M., Yamazaki M., Sudiyama T., Irie R., Otsuki T., Sato H., Wakamatzaki M., Sudiyama T., Irie R., Kawai Hio Y., Saito H., Walahkawa T., Kimura K., Yamashita H., Marakuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Yamasuo K., Nakamura Y., Sujiyama A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human CDNA sequencing project.";

"NEDO human CDNA sequencing project.";
Submitted (COT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AROS5636; BAB7097661.".

SEQUENCE 245 AA; 26111 MW; BIAB6EBDAZEBEE06 CRC64;
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNERPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
6DNA FLJ31074 FIS, CLONE HSYRA2001476.
Homo sapiens (Human).
6DNA FLJ31074 FIS, CLONE GARAIA: Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.
Ouery Match 33.7%; Score 582; DB 4; Length 245; Best Local Similarity 48.4%; Pred. No. 2.2e-42; Matches 124; Conservative 47; Mismatches 71; Indels 14;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 467; DB 4; Length 97; Pred. No. 5.4e-33; 0; Mismatches 4; Indels
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                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
TISSUE-BREAST, AND MAMMARY ADENOCARCINOMA;
Strausberg R.;
Strausberg R.;
Submitted (AGG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012475; AAH12475.1; -...... 14F475F0B170E71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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9.2%; Score 159.5; DB 11;
Best Local Similarity 27.9%; Pred. No. 6.2e-05;
Matches 63; Conservative 41; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 VSMNDGLSFISSSVIITTTHCSLHKIASGPTTAACME 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00242; INTEGRIN_ALPHA; 1. PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pram: PF00092; vwa: 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM0191; INt_alpha; 4.
SMART; SM00327; VWA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.0%;
95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.93
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Q9BPQ8 Q9BPQ8;

RESULT

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DEVENDED 149203; PubMed-8426611; MEDELINE-93149203; PubMed-11, Hug D., Huembelin M., Weber G.; Pasamontes L.E., Hug D., Huembelin M., Weber G.; Sequence of a major Eineria maxima antigen homologous to the Eimeria "Sequence of a major Eineria".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 ---ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP--VNDGFQALQGIIHSI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         004588;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR ANTIGEN HOMOLOGOUS SEQUENCE (EMP100).
Elmeria maxima.
Elwaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Elmeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eimeria tenella.
Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
Eimeria.
NCBI_TaxID=5802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGGPACYGGFDLYFILDKSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 VLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSERE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75808 MW; AC2A0E7A346A7E9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           043981;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MICRONEME PROTEIN ETMIC-1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.7%; Score 150.5; DB 5; Best Local Similarity 25.9%; Pred. No. 0.0002; Matches 69; Conservative 45; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     712 AA
                                                                                                                       724 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tenella microneme protein Etp100.";
Mol. Biochem. Parasitol. 57:171-174(1993).
EMBL; M99058; AAA29076.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR00035; WWFA.
Pfam: PF00090; tsp_1: 6.
Pfam: PF00092; wwa: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 LKKSCIEI----LAAEPSTI--CAGE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00453; VWFADOMAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50092; TSP1; 5.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 724 AA; 75808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     043981
                                                                                                                       004588
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Q04588
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X MEDLINE-21103187; PubMed-11160215;

X MIYAZAWA S., Azumi K., Nonaka M.;

MIYAZAWA S., Azumi K., Nonaka M.;

T "Cloning and characterization of integrin alpha subunits from the solitary ascidian, Halocynthia roretzi.";

L J. Immunol. 166:1710-1715(2001).

E MEMBL: AB048261; BAB21479.1; -.

R RSP: P11215; 1A84.

R InterPro; IPR000413; Integrin_alpha.

R InterPro; IPR002035; vWFA.

R Pfam; PF01839; FG-684; 5.

R Pfam; PF01837; integrin_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 VFSTRGTTLMKLTEDREQIRQGLEELQKVLPG-------GDTYMHEGFERAS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 ------AKLDIGKEIVRVGVVQYSHYVEGKSINKQKYITTEISIGEFKLLDNFENAV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDLGAIVYCVGVKDFNETQLARIA---DSKDHVFPVNDGFQALQGIIHSILKKSCIEILA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 DPQSLVDPIVQLQ----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GGRREDGG-----PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFI 83
                                                           157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.9%; Score 153.5; DB 5; Length 1332; 24.1%; Pred. No. 0.00025;
live 42; Mismatches 81; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
INTEGRIN ALPHA HR1.
W; 0D9108D2B05CFFAE CRC64;
                                                                                                                                                                             208 LOGIIHSILKKSCIEILAAEPSTICAGESFOVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                      Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIN ALPHA HRI PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                Ş
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SEQUENCE 1332 AA; 145852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ::: | | | 398 GGKSAKTAG--YEMHFGENGF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEPSTICAGESFQVVVRGNGF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Local

Best Loc Matches

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129

169

q

Signal.

17;

Gaps

43;

Length Indels

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EMBL, AF10906; AAC84162.1; --
EMBL, AF10906; AAC84162.1; --
EMBL, BC01108; AAH11086.1; --
HSSP; DO0761; IEPT.
MGD, MGI:88226; C2.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00135; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR002035; VWFA.
Pfam; PF00089; trypsin; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PR00725; CHYMOTRYPSIN.
PRINTS; PR00453; VWRAPDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                          SWART; SM00032; CCP; 2.
SWART; SM00020; Tryp_SPC; 1.
SWART; SM00120; Tryp_SPC; 1.
SWART; SM00120; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 2.
PROSITE; PS00135; TRYPSIN_ER; UN
PROSITE; PS00135; TRYPSIN_ER; UN
PROSITE; PS00234; VWFA; 2.
Hydrolase; Serine procease.
SEQUENCE 760 AA; 84741 MW; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 MND-----GLSFISSSVII 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.8%
Best Local Similarity 23.5%
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                             SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
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Q9U8J9
ID Q91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP-----VNDGFQ 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 PKATNPSLAISAARSLSYSTGVIYTHYGLQDA-KKLLYDINAGARNNVPKLVLVMTDGA- 164
                       MEDLINE=92131064; PubMed=1775171;
MEDLINE=92131064, PubMed=1775171;
Tonley F.M., Clarke L.E., Kawazoe U., Dijkema R., Kok J.J.;
"Sequence of the gene encoding an immunodominant microneme protein of Eimeria tenella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mariata; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                            A Kelleher M., Tomley F.M.;
A Kelleher M., Tomley F.M.;
A Kelleher M., Tomley F.M.;
Translated expression of beta-galactosidase in differentiating sporozoites of Elmeria tenella.";
L. Mol. Blochem. Parasitol. 97:21-31(1998).
E. EMBL, AF032905; AAD03350.1; -..
R. EMBL, AF032905; AAD03350.1; -..
R. Interpo. IPR000884; TSP1.
R. Interpo. IPR000909; vWPA.
R. Pfam: PF00090; vwa: 1. 6.
R. Pfam: PR00090; vwa: 1.
R. PRINTS; PR00453; vwa: 1.
R. SMART; SM00209; TSP1: 6.
R. RART; SM00209; TSP1: 6.
R. RART; SM00209; TSP1: 6.
R. RART; SM00209; TSP1: 6.
R. PROSITE; PS50024; VWPA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                            ch 8.0%; Score 137.5; DB 5; Length 712; 1 Similarity 24.7%; Pred. No. 0.0025; 67; Conservative 43; Mismatches 108; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S).
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
MICRONEME PROTEIN ETMIC-1.
15B8F3C190B70F73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 ALQGIIHSILKKSCIEILAAEPSTI--CAGE 235
                                                                                Mol. Biochem. Parasitol. 49:277-288(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                 36 PO
712 MI
74777 MW;
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37 7
712 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 67; Conserv
                                                                                                     [2]
SEOUENCE FROM N.A.
        SEQUENCE FROM N.A.
                                                                                                                             STRAIN-HOUGHTON;
MEDLINE-99094493;
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SEQUENCE
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183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----KD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 ERSQ-----DVTEVITSLDSASYRDHENATGINIYEVLIRVYSMMQSQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; "Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVSVAIITFASQPKTIMSILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-------NRQGYRTAS-
                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. submitted (JUL-2001) to the EMBL/GenBank/IDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
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G
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                                                                                                                               [2]
SEQUENCE OF 291-760 FROM N.A.
Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas
                                                                                                                                                                                                           Hood L.; submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91C896A3EDC7D448 CRC64;
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193 FTLKKFTKVEDII-----EAINTFPYRGGSTNTGKAMTYVREKIFVPSK-GSRSNVPKVM 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 TTLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVND 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 CYGGFDL---YFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2000 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ234P15.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT).
COL12A1.
COL12A1.
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.6%; Score 131.5; DB 4; Length 517; Best Local Similarity 29.6%; Pred. No. 0.0054; Matches 61; Conservative 39; Mismatches 77; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Smith M.; | Smith M.; | Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. | Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. | EMBL, ALOBO250; CAB65984.1; -.. | FASP: P11215; IBHQ. | InterPro; IPR003961; FN_III. | InterPro; IPR002035; vWFA. | InterPro; IPR002035; vWFA. | Pfam; PF00041; fn3; 2. | PR0041; fn3; 2. | PR00453; vW#ABOMAIN. | PRINTS; PR00453; vW#ABOMAIN. | PRINTS; PR00560; FN3; 2. | SMART; SM00260; FN3; 2. | SMART; SM00260; FN3; 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SM00273, vWA3, 2. | SMART; SMART; SMART; SMART; SMART; SMART; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72523 MW; 3E3A10A285ECAA51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                517
56727 MW; 9B6972F44A1BD88F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 -FDAFQRISFELTQSICLRIEQELAA 327
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                                                        Interpro; IPR003961; FN_III.
Interpro; IPR002035; WFA.
Pfam; PF00041; fi3; 3.
Pfam; PF00092; wwa; 1.
PRINTS; PR00453; WWFADOMAIN.
SMART; SM00060; FN3; 3.
SMART; SM00327; WWA; 1.
U68139; AAC01506.1; -. P17301; 1AOX.
                                                                                                                                                                                                                                                                           PROSITE; PS50234; VWFA; 1.
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                                                                                                                                                                                                               Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida, Sarcocystidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 CTSQLDICFLVDSSGSIGEAHYEE----VRQFLHAFLSKLPIGNDEVNTSLVIFSTTVHP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 LMKL----TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY-YENRQGYRTASVII 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF-NETQLARIADSKDHVFP----V 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CYGGFDLYFILDKSGSVLH-HWNEIYYFVEQLAHKFIS-----PQLRMSFIVFSTRGTT 91
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20183852: PubMed-10717300;
MEDLINE-20183852: PubMed-10717300;
Molecular characterization of a LD.;
Molecular characterization of a LD.;
protein homologue in Neospora canium.";
Mol. Biochem. Parasitol. 107:33-43(2000).
EMBL, AF061273; AAF01565.1;
InterPro; IPR001969; ASP_protease.
InterPro; IPR001969; ASP_protease.
InterPro; IPR001969; WFA.
Pfam; PF00090; tsp_1:
Pfam; PF00090; tsp_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match ' 7.7%; Score 132.5; DB 5; Length 765; Best Local Similarity 25.1%; Pred. No. 0.0076; Matches 50; Conservative 35; Mismatches 89; Indels 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  765 AA; 82880 MW; 9727838CC1FE8CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TYPE XII COLLAGEN (FRAGMENT).
                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THROMBOSPONDIN-RELATED ADHESIVE PROTEIN HOWOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
PROSITE; PS50092; TSP1; 6.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 765 AA; 82880 MW; 9727838CC1F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 NDGFQALQGIIHSILKKSC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 QTEWSOLLPSISPILKEVC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00453; WWFADOMAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=29176;
                                                                                                                                                                                      Neospora caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-CORNEA;
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6 6 6

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PRT; 3767 AA.

PRELIMINARY;

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021340;
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SEQUENCE
                                                                                                                               STRAIN=N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 -TASVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FN----ETQLARIA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 -------REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYR- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 THFTENDFKRNPSPKLLVRPIRQLL------GRTHTATGIRKVVRELFH-SKSGARE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 NALKILVVITDGEKFGDPLGYEDVIPEADRK---GVIRYVIGVGDAFNSWKSREELNTIA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 DSK--DHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKPCGDHVFQVNN-FEAVKTIQNQLQEKT----FAIEGTQTGSTSSFECEMSQEGFSAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISP---QLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI 211
           DREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 153
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. NCBI_TaxID=9823;
DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE
                                                 Length 920;
                                                                                                                                                                                                                                                                                                    Lee J.-K., Schook L.B., Rutherford M.S.;
Lee J.-K., Schook L.B., Rutherford M.S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
REMEL: U40072; AAB16869.1; -.
HSSP, P11215; 1A8X.
HSSP, P11215; 1A8X.
InterPro; 1PR00133; Integrin_alpha.
InterPro; 1PR00133; VWFA.
Pfam; PF00183; VWFA.
Pfam; PF00183; VWFADOMAIN.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR0013; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00127; VWA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                102440 MW; E96CC51E350DD5AC CRC64;
                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.6%; Score 130.5; DB 6;
26.4%; Pred. No. 0.015;
:ive 41; Mismatches 72;
                                                                                                                                                                                 920 AA
                                                                                                                                                                                                      Created)
                                                                                                                                                                                   PRT;
                                                                                                                                                                                              01-000'1996 (TrEMBLrel. 01, C1
01-FEB-1997 (TrEMBLrel. 02, LE
01-FEC-2001 (TrEMBLrel. 19, La
CD11B (FRAGMENT).
                                                                                                                   212 IHSILKKSCIEI---LAA 226
                                                                                                                              PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 AA;
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Matches 63; Conserv
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   Sus scrofa (Pig).
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NON_TER
SEQUENCE
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RESULT Q9UA13

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TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TREMBLrel. 19, Last annotation update)
TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-3 PRECURSOR (K08E5.3 PROTEIN)
                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like domain; Glycoprotein; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8DA3AE5EA50AEB8E CRC64;
                                                                                                                                                                                                                                                                                                                        Lu 2., Vogel B., Hedgecock E.; "una 2., Nogel B., Hedgecock E.; "mua 2., RNNA Splicing Pattern Revealed."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kershaw J.K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMO0181; EGF. 51.

SMART; SMO0179; EGF_CA; 1.

SMART; SMO0179; EGF_CA; 1.

SMART; SMO0192; EGF_LIKe; 45.

SMART; SMO0200; SEA; 2.

SMART; SMO0207; VWA; 1.

PROSTITE; PSO0010; ASX_HYDROXXL; UNKNOWN_32.

PROSTITE; PSO1010; ASX_HYDROXXL; UNKNOWN_1.

PROSTITE; PSO1186; EGF_2; 6.

PROSTITE; PSO1187; EGF_CA; 1.

PROSTITE; PSO1068; LDLRA_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nask; vulla, luncary, luncary, lenterpro; lengolofs; bask_hydroxyl.
Interpro; lengolofs; bishtegrin.
Interpro; lengolofs; bgF-like.
Interpro; lengolofs; bgF-cept_A.
Interpro; lengolofs; seA.
Interpro; lengologs; seA.
Interpro; lengologs; seA.
Pfam; pro0008; EGF; 33.
Pfam; pro01390; SEA; 2.
Pfam; pro01390; seA; 2.
Pfam; pro01390; seA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating blology.";
Science 282:2012-2018(1998).
EMBL; AF139060; AAD29428-1;
EMBL; 230974; CAA83226.2; JOINED.
HSSP; P01130; 1LDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00289; DISINTEGRIN. PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO1187; EGF_CA; 1
PROSITE; PS50068; IDLRA_2;
PROSITE; PS50024; SEA; 4.
PROSITE; PS50234; VWFA; 2.
Calcium-binding; EGF-like of
Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3767
' AA;
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>3767
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Best Local Similarity
Matches 64; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
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3767
                                                                                                                                     MUA-3 OR K08E5.3
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---DLYFILDKSGSVLHH--WNEIYYFVEQLA 70

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NON_TER
SEQUENCE
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ELFEIGRSKTRVGLIQYSDQIRHEFDLDQYGDRDSLLKGISETQ-YLTGLTRTGAAIQHM 1317
                                                                                                                                   1318 VQEGF----TGPADSARKLSIN 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 DGELHEDLFFYSEREANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFPVN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                                                       01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-087-2001 (TrEMBLrel. 19, Last senotation update)
INTEGRIN BETA 2 ALPHA SUBUNIT.
Rattus norvegicus (Rat)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 NIAFLIDGSGSI-----INTIDF----QKMKEFVSTVMDQFQKSKTLFS-----LMQYSDEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THETENDEKRNPDPKSHVRPIRQLNGRTKTASGIRKVVRELFQKINGARDNAAKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 DGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKIN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                     ::|| | ::| || |: | || || 1365 TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS 1413
                                          71 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                                                                                  175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 --ITSN-------GPLLGSVGSFDWAGGAFLYPSKDKASFINTTRI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 DSVTLNEKPFSVEDTYLLCPAPILKEVG----MKAALQVSMNDGLSFISSSVI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 123; DB 11; Length 11:
23.9%; Pred. No. 0.088;
Live 46; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fathallah D.M. Sr., Zerria K. Jr.;
"Cloning of the rat CDID cDNA sequence.";
"Cloning of the rat CDID cDNA sequence.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF268593; AAF81280.1;
"HSSP; P11215; IAAX.
InterPro; IPR004013; Integrin_alpha.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;
                                                                                                                                                                                                                                                                               PRT; 1151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00092; vwa; 1.
PRINTS: PR0118PS: INTECRINA.
PRINTS: PR00453; VWEADOMAIN.
SMART: SM00191; Int_alpha; 5.
SMART: SM00327; VWA; 1.
PR0SITE: PS00442: INTECRIN_ALPHA; 1.
PR0SITE; PS50234; VWFA; 1.
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Pfam; PF00357; integrin_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.99
Matches 70; Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                        TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 EKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AA; 24505 MW; 31AB702E42E9CEB3 CRC64;
                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 24.5 KDA PROTEIN (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 121; DB 11
44.0%; Pred. No. 0.014;
iive 11; Mismatches 1
221 AA
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                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001) to the EMBL; BC003908; AAH03908.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.09
Matches 22; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August
Job time: 849 sec
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                         Strausberg R.;
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us-09-970-076-8.rspt

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(without alignments) 518.350 Million cell updates/sec
                                                                                                             Search time 61.73 Seconds
                                                                                                                                                                                                      1728
1 MATAERRALGIGFQWLSLAT.....TTHCSLHKIASGPTTAACME
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                   283138 segs, 96089334 residues
                                                                                                             ••

    protein search, using sw model

                                                                                                           9, 2002, 10:34:18
                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                             August
                                                                                                                                                                                                      Perfect score:
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                                                                          OM protein
                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                             Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

leukocyte surface immunodominant mic collagen alpha 1(X classical-compleme collagen alpha 1(X collagen alpha 1(X hypothetical prote cartilage matrix p type XII collagen complement factor antigen Em100 - Ei cell surface glyco cell surface glyco collagen alpha 1(V complement factor collagen alpha 2(V hypothetical prote hypothetical prote hypothetical prote dnak protein (heat hypothetical prote cartilage matrix p cartilage matrix p hypothetical prote collagen alpha 1(X sporozoite surface rop protein - frui thrombospondin-rel factor Description complement SUMMARIES BBHU A54849 BBMS S21369 S66522 A33809 I51579 A48569 RWHU1B RWHU1C A40020 S00551 A45638 C2MS S31212 S78476 S42373 A37979 I51027 A46283 T23087 T04822 S33578 S04531 B96958 T46488 T28797 E70121 Query Match Length DB 760 1857 1888 3051 496 929 764 761 1029 500 747 747 1450.5 1445.5 1445.5 1441.3 137.5 1310.5 131 Score . 8

RESULT

kinesin-like prote collagen alpha 2(v collagen alpha 2(v collagen alpha 2(v collagen alpha 3(v imidazolonepropion dhak protein NMBO5 collagen alpha-1 probable retroelem transcription regu arginyl-tkn synth inter-alpha inhibi integrin alpha-E c	integrin alpha-1 c undulin 1 - human
T50240 S09646 CGHU2A CGHU2A D87368 H81185 A37797 T47637 A53248 A53248 A53248 A53248 A53248 A53248 A53248	A45226 A40970
000000000000000000000000000000000000000	N 0.
817 917 1018 3176 401 642 3137 676 689 932 1179	1151 843
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99999999999999999999999999999999999999	94.5 94
011264500000001126	4 4 5

ALIGNMENTS

A48569

283138

hits satisfying chosen parameters:

Total number of

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Autoros Elmeria maxima
C; Species: Elmeria maxima
C; Species: Elmeria maxima
C; Species: Elmeria maxima
C; Species: Elmeria maxima
C; Species: Elmeria maxima
C; Date: 0.1-0ec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C; Accession: 448569
R; Päsamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
A; Title: Sequence of a major Elmeria maxima antigen homologous to the Elmeria tenella A; Reference number: A48569; MuID: 93149203
A; Title: Sequence of a major Elmeria maxima antigen homologous to the Elmeria tenella A; Reference number: A48569; MuID: 93149203
A; Accession: A48569
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-724 <PAS.
A; Cross-references: GB:M99058; NID: 9158890; PID: 9158891
A; Residues: 1-724 <PAS.
A; Cross-references: GB:M99058; NID: 9158890; PID: 9158891
A; Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
C; Superfamily: thrombospondin type I repeat homology <THR1>
F; 332-296, Domain: thrombospondin type I repeat homology <THR2>
F; 332-296, Domain: thrombospondin type I repeat homology <THR3>
F; 343-493/Domain: thrombospondin type I repeat homology <THR4>
F; 560-610, Domain: thrombospondin type I repeat homology <THR6>
F; 560-610, Domain: thrombospondin type I repeat homology <THR6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.7%; Score 150.5; DB 2; Best Local Similarity 25.9%; Pred. No. 0.00032; Matches 69; Conservative 45; Mismatches 109;
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A; Title: Characterization of the myeloid-specific CD11b promoter. A; Reference number: 152567; MUID:92144986
A; Accession: 152567
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A,Rolecule type: MRNA
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B, Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
R,Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
R,Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
A,Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor
A,Rocession: A3218; MUD:89098893
A,Residues: J-1153 AGIO4145; NID:9189068; PIDN:AAA59903.1; PID:9386975
A; Mocie; Part of this sequence was oonfirmed by protein sequencing
A; Mocie; Part of this sequence was oonfirmed by protein sequencing
A; Mocie; Part of this sequence was oonfirmed by protein sequencing
A; Mocie; Part of this sequence was oonfirmed by protein sequencing
A; Accession: A6526
A; Reference number: A6526; MUD:93123748
A; Reference number: A6526; MUD:93123748
A; Residues: 1-499. 501-113; PED:3263047; PIDN:AAB24821.1; PID:9263049
A; Mocession: A6526
A; Accession: A6526
A; Moces: Sequence cracked from NCBIP backbone (NCBIP:121963)
A; Moces: the last three bases of intron 13, CAG, are included in some but not all mature
A; Note: sequence cracked from NCBIP backbone (NCBIP:121963)
A; Reference number: A90664; MUD:9706671
A; Residues: 17-31 Remoid-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
A; Residues: A6019
A; Residues: A6019
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A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Residues: 1-499,501-965,'P',967-1153 <ARN>
A; Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A; Note: the authors translated the codon TAC for residue 1129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was confin
A; Note: part of this sequence, including the amino end of the mature protein, was confin
B; Shellow, C.S.; Arnaout, M.A.
B; Shellow, Acad. Sci. U.S.A.
B; Reference number: A41600; MUID:92073318
A; Residues: 1-9 SSHES.
A; Residues: 1-9 SSHES.
A; Residues: 1-9 SSHES.
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R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A;Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi A;Reference number: A94193; MUID:88190151
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A; Rolecule type: mRNA
A; Residues: 1-1153 <CON5
A; Cross-references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Cross-references: GB:J03925; NID:g187284; PIDN:AA59544.1; PID:g307148
A; Cross-references: GB:J03925; NID:g187284; PIDN:AA59544.1; PID:g307148
A; Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
A; Trile: Anino acid sequence of the alpha subunit of human leukocyte adhesion receptor
A; Reference number: A28915; MUID:88257215
                                                           A; Reference number: A31108; MUID: 88315033
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COMM:120980
A,Genetics:
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A,Map position:
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C,Superfamily:
C=1 surface glycoprotein CD11b; von Willebrand factor type A repeat h
A,Note:
C,Superfamily:
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                                                                                                                                      A; Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C; Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 ------REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 149
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R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 FTFKEFQNNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.4%; Score 145.5; DB 1;
illarity 26.2%; Pred. No. 0.0015;
Conservative 45; Mismatches 81;
A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-834 <CO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 60; Conserv
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us-09-970-076-8.rpr

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C:Generics:
A:Introns: 2845/3; 2863/3; 2863/3; 2863/3; 2863/1; 2985/1; 2985/1; 3008/1; 3065/1
C:Superfamily: collagen alpha 1(XII) chain: fibromectin type III repeat homology; von C:Superfamily: collagen alpha 1(XII) chain status predicted call: connective tissue; disul F;1-23/Domain: signal sequence *status predicted call: connective tissue; disul F;1-23/Domain: signal sequence *status predicted call: connective tissue; disul F;1-13/Domain: signal sequence *status predicted call: collagen alpha 1(XII) chain short splice form *status predicted call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: call: ca
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F;32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Blnding site: carbohydrate (Asn) (c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: $23814
A; MoLecule type: protein
A; MoLecule type: protein
A; Residues: 'X',1333,'O',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
R; Dublet, B.; van der Rest, M.
J. Blod. Chem. 262, 17724-17727, 1987
J. Blod. Chem. 262, 17724-1777, 1987
A; Reference number: $22254; MUID: 88087065
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDN
A;Reference number: A28037; MUID:87317590
                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 2960-2976, Fr. 2978-3074, AG' <GOR3>
A; Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1; PID:g211650
A; Note: this sequence has been revised in reference A34485
R; Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Blochem. 207, 847-856, 1992
Eur. J. Blochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel large form
A; Reference number: $23814; MUID:92362621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S22254
A; Molecule type: protein
A; Residues: 2831-2832, Tr', 2834, 'R', 2836-2843; 3002-3014 < DUB>
B; Trueb, J: Trueb, B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A; Title: The two splice variants of collagen XII share a common 5'
A; Reference number: S28811; MUID:93042014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-collagenous NC2 #status predicted <NC2> collagenous COL1 #status predicted <COL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collagenous COL2 #status predicted <COL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A) Cross-references: EMBL:X6737
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell attachment (R-G-D) moti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S28811
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51-2902/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :2903-2945/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;2899-2901/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Access-references: GDB:119758; OMIM:151510
A:Wap position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo C:Reywords: calcium; calcium; dahesion; glycoprotein; heterodimer; magnesium; tandem repeat; E:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1103/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:20-1103/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:149-319/Domain: extracellular #status predicted <EXT>
F:149-319/Domain: von Willebrand factor type A repeat homology <WWA4>
F:1108-1133/Pomain: transmembrane #status predicted <TWN>
F:1134-1163/Domain: intracellular #status predicted <TWN>
F:1134-1163/Domain: ditracellular #status predicted <INT>
F:61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A40000
A; Accession: A40000
A; Molecule type: mRNA
A; Residues: 1-3124 < YAM5
A; Cross-references: GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A; Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and, B; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A; Title: Type XII collagen. A large multidomain molecule with partial homology to type I A; Reference number: A34485; MUID:90062079
                                                                                                                                                             A; Wolecule type: mRNA
A; Residues: 1-755, 'L', 757-1163 <CO3>
A; Cross-references: GB: M81695; EMBL: Y00093; NID: 9487829; PIDN: AAA59180.1; PID: 9487830
A; Cross-references: GB: M81695; EMBL: Y00093; NID: 9487829; PIDN: AAA59180.1; PID: 9487830
A; Note: part of this sequence was confirmed by protein sequencing
C; Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on my C; Genetics:
A; Gene: GDB: ITGAX; CD11C
                                               structure of the alpha subunit of a leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Tille: The complete primary structure of type XII collagen shows a chimeric molecule wones region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site. A;Reference number: A40020; MUID:92011862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Oba.
J. Cell Biol. 115, 209-221, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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A;Residues: 2456-2738,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross.references: EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PID:9211285
A;Accession: B34485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 DIVELIDGSGSISSRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEEFRRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KDFNETQLARIAD--SKDHVFPVNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 FQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 FDALKDIQNQLKEK----IFAIEGTETTSSSSFELEMAQEGF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 143.5; DB 1;
; Pred. No. 0.0023;
43; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 1(XII) chain precursor - chicken N; Alternate names: fibrochimerin
                                      A, Title: CDNA cloning and complete primary A, Reference number: S00864; MUID:88166645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 2772-2792; 2846-2873 <GOR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 LFFYSEREANRSRDLGAIVYCVGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                     Accession: S00864
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A45038
Immunodominant microneme protein Etp100 - Eimeria tenella
C;Species: Eimeria tenella
C;Species: Eimeria tenella
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
R;TomLey, F.M.: Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria A;Teference number: A45538
A;Acteres: preliminary
A;Acteres: preliminary
A;Acteres: preliminary
A;Gross references: GB:AF032905; GB:M73495; NID:92707732; PIDN:AAD03350.1; PID:927077
A;Cross references: GB:AF032905; GB:M73495; NID:92707732; NCBIP:77750
A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
A;Note: sequence extracted from NCBI repeat homology <THR2>
F;38-296/Domain: thrombospondin type 1 repeat homology <THR2>
F;39-31/Domain: thrombospondin type 1 repeat homology <THR3>
F;39-31/Domain: thrombospondin type 1 repeat homology <THR3>
F;48-34-556/Domain: thrombospondin type 1 repeat homology <THR3>
F;48-456/Domain: thrombospondin type 1 repeat homology <THR3>
F;48-456/Domain: thrombospondin type 1 repeat homology <THR3>
F;560-610/Domain: thrombospondin type 1 repeat homology <THR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 1(XIV) chain precursor, short form 2 - chicken N;Alternate names: undulin (S;Species: Gallus agallus (chicken) (C;Species: Gallus agallus (chicken) (C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 (S;Accession: A45974; S30085; S22916; S17035; S20833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 -SNLPSQTRSSAAALRDAGALVVVLGVGSGVNSSECRSIAGCSTSNCPRYLQSNWSNVTQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQKVLPG------GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGEL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDREQIRQGLEE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 PKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLVLVMTDGA- 164
                                                                                                                                                                                VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
                                                                                           154 HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP-----VNDGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAPLPRRRIA---PCRALSLIVGLLAASFAFSSLOPGATTSSGODOVCTSLLDVMLVVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK
                                                           DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP
198 IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT
                                                                                                                                                                                                                                                                                                                                       356 -SASITSN------GPLLGSVGSFDWAGGAFLYTSKDKVTFINTT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 712;
                                                                                                                                                                                                                                                                                                     261 INDSVTLNEKPFSVEDTYLLCPAPILKEVG----MKAALQVSMNDGLSFISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                         ; Score 137.5; DB 2;
; Pred. No. 0.0036;
43; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALQGIIHSILKKSCIEILAAEPSTI--CAGE 235
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Local Similarity 24.7%;
hes 67; Conservative 4
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C; Species; Nus musculus (house mouse)

C; Accession: S00551; 159078

R; Pytela, A. Mino acid sequence_revision 30-Sep-1991 #text_change 22-Oct-1999

R; Pytela, A. Mino acid sequence of the murine Mac-1 alpha chain reveals homology with the i A; Accession: S00551; MUID:88312584

A; Molecule type: DNA

A; Reference number: S00551; MUID:88312584

A; Molecule 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Residues: 1-1153 < PyTP

A; Reference number: 159078; MUID:86287312

A; Reference number: 159078

A; Reference number: 159078

A; Residues: 1-144 < RRES

A; Residues: 1-144 < RRES

C; Genetics: A; Gene: Mac-1

C; Superfamily: cell surface glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein

C; Reywords: cell adhesion; glycoprotein; transmembrane protein
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                      F;2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (Pro) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 DIVFLIDGSGSI----NNIDF---QKMKEFVSTVMEQFKKSKTLFS-----LMQYSDEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                          QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 AF---KEPAIKLRDADVEIFAVGVKDAVRTELEAIASPPAETHVYTVED-FDAFQRISFE 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1153;
                                                                                                                    Length 3124;
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                                                                                                                       ; Score 143; DB 1;
; Pred. No. 0.0093;
51; Mismatches 97,
                                                                                                                                    8.3%;
26.1%;
                                                                                                                                                                                         Conservative
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---EKSYLI 663
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                                                                                                                                                                   Similarity
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component precursor

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F.156-210/Domain: Complement factor H repeat homology FH35
F.156-210/Domain: Complement factor H repeat homology FF.251-760/Product: Complement C2a fragment long form #status predicted <C2s>F.251-760/Product: Complement C2a fragment short form #status predicted <C2s>F.259-449/Domain: von Willebrand factor type A repeat homology FF.478-747/Domain: trypsin homology #status atypical <TRY>
F.226-449/Pomain: Lypsin homology #status atypical <TRY>
F.226-449/Pomain: trypsin homology #status atypical FF.270-737,340,474.478,663/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.511,570,689/Active site: His, Asp, Ser #status predicted
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C. Superfamily: complement C. Superfamily: complement C. Superfamily: complement C. Superfamily: complement C. Superfamily: duplication; glycopro
C. Keywords: alternative splicing; complement classical pathway; duplication; glycopro
F.1-18/Domain: signal sequence #status predicted <SIG>
F.19-28/Domain: complement C.D fragment #status predicted <C2B>
F.22-89/Domain: complement factor H repeat homology <FH1>
F.94-149/Domain: complement factor H repeat homology <FH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-760 <123-
A; Cross-references: GB:M57891; GB:J05661; NID:9192436; PIDN:AAA63294.1; PID:9192437
A; Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R.
B; Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R.
A; Ishikawa, N.; Nonaka, M.; Metsel, R.A.; Golten, H.R.
A; Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different
A; Reference number: A36593; MUID:91035430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actross references: EMBL:MS7891; NID:q192436; PIDN:AAA63294.1; PID:q192437
Actross references EMBL:MS7891; NID:q192436; PIDN:AAA63294.1; PID:q192437
By:Falus, A.; Wakeland, E.K.; McConnell, T.J.; Gitlin, J.; Whitehead, A.S.; Colten, Immunogenetics 25, 290-298, 1987
A.Title: DNA polymorphism of MHC III genes in inbred and wild mouse strains. A; Reference number: 154429; MUID:87192938
A;Accession: I54429
A;Accession: I54429
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 660-677, R',679,681-723, 'G',725 <RES>
A;Cross-references: GB:M16271; NID:q199289; PIDN:AAA39562.1; PID:q199290
C;Genetics: A
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                                                                                                                                                                                                                                                                                                                            classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C2 component pr N.Alternate names: C3 convertase; C5 convertase; complement C2 (5.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000 C.Accession: A38876; B36593; I54429 R.Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R. submitted to GenBank, January 1991 A.Reference number: A38875 A.Reference number: A38876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 KEIRHTIILLTDGK--SNAGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE 429
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A; Residues: 1-760 <ISH>
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1151 NVYPCYRL 1158
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               SVEDTYLL
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R;Gerecke, D.R.; FOley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Status: preliminary
A.Status: mRNA
A.Molecule type: mRNA
A.Residues: 286-494, '0',496-834, 'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
R.Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne,
R.Bordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne,
R.Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, A.; Mayne,
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A;Reference number: S17035; MUID:92037885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A) Experimental source: embryo skin

A) Experimental source: embryo skin

A) Note: sequence inconsistent with the nucleotide translation

A) Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)

B) Submitted to the EMBL Data Library, March 1992

A) Reference number: S30085

A) Recession: S30085

A) Nolecule type: mRNA

A) Residues: 1472-1660 <APT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-rences: EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175
R;Trueb, J.; Trueb, B.
Eur. J. Blochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443
A;Accession: S22916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1554-1659/Domain: triple helical domain COL1 #Status predicted <COL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF
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A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
                                                                                                                                                                                                      A; Reference number: A45974; MUID:93280195
                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-1747 <GER>
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A; Residues: 1472-1659 <GOR1>
A; Accession: S20833
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                                                                                                                                                                                                                                                              A; Accession: A4597
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A; Accession: S/44/b
A; Molecule type: mRNA
A; Residues: 1-1888 G-TRU>
A; Cross-references: EMBL:X70793; NID:9288872; PIDN:CAA50064.1; PID:9288873
A; Cross-references: EMBL:X70793; NID:9288872; PIDN:CAA50064.1; PID:9288873
A; Cross-references: EMBL:X70793
A; Title: Complete primary structure of chicken collagen XIV.
A; Fitle: Complete primary structure of chicken collagen XIV.
A; Reference number: S31211
A; Recession: S31211

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C.Species: Caenorhabditis elegans
C.Species: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C.Saccession: S42373
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collagen alpha 1(XIV) chain precursor, long form - chicken collagen alpha 1(XIV) chain precursor, long form - chicken callus gallus (chicken) c.species: Gallus gallus (chicken) c.har-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999 c.hacession: S78476; S31211
R.Trueb, B. Submitted to the EMBL Data Library, January 1993 h.Reference number: S78476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
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Best Local Similarity 25.0%; Pred. No. 0.055;
Matches 62; Conservative 44; Mismatches 116; Indels
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hypothetical protein T20G5.3 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1267 NVYPCYRL 1274
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: 531212
Eur: J: Riadelphi, C.; Trutubb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reteacen unmber: 531211; MUID:9318568
A;Accession: 53122
A;Accession: 53122
A;Accession: 53122
A;Accession: 53124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1042 DLVFLVDGSWSIGDDNFNKIISFLXSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 97
                                                                                                                                                                                                                                GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII
                            FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
                                                                             7.5%; Score 130; DB 2; Length 1857; 25.0%; Pred. No. 0.054; trive 44; Mismatches 116; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                                                                                                                                                                                                                                                           299 MND-----GLSFISSSVII 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
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1267 NVYPCYRL 1274
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NyAlternate names: C3 convertase; C3 proact incurr; glycine-rich beta-glycoprotein; he NyContains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragmen C5 Specias: Homo sapiens (man) C5 Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000 C; Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339; A44628; SXMella, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G. Abbitted to the EMBL Data Library, March 1993 A; Reference number: S34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cypexit collagen alpha-1 chain - eastern newt (fragment)
Cypexies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cypecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cypecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cypecssion: 151027
R;Wei, Y; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Fitle: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII
A;Reference number: 151027; MUID:95246925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g632648 C;Superfamily: collagen alpha I(XII) chain; fibronectin type III repeat homology: F;155-236/Domain: fibronectin type III repeat homology <3FR-F;F;F;F;795/Pomain: von Willebrand factor type A repeat homology <WWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 DIVLLVDGSWSIGRPNFKIVRNFISRVVEVFDIGSDRVQIAVSQYSGDPRTEWQLNTHKT 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 102
                                                                                                                                                                                                                                                                                       315 GLVQYSSSVROEFPLGRFHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSF 366
                                                                                                                                                                                                                                                   134 ENRQGYRTAS--VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
81
                                                                                                                                                                                                                                                                                                                                                                                                                                     472
                                                                                                                                                                                                                                                                                                                                                                           192 ADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP
                                      RQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI
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                                                                                                                           82 FIV----FSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y
ICAGGGGRREDGGPACYGGFDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMS
                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 118; DB 2; Length 929;
21.2%; Pred. No. 0.2;
tive 51; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: 151027
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA
A; Residues: 1-929 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement factor B precursor [validated] - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 --- OEVYVRGTQTTTVLVGLKPETEYYVN 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 6.8%
Best Local Similarity 21.2%
Matches 57; Conservative
                                                                264 VCSGGGGS----
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A: Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C: Complex: homotrimer
C: Superfamily: unassigned EGF-related proteins; EGF homology; won Willebrand factor type C: Keywords: glycoprotein; homotrimer
F: 1-22/Domain: signal sequence #status predicted <SIG>F: 23-496/Product: cartilage matrix protein #status predicted <NAT>F: 39-206/Domain: von Willebrand factor type A repeat homology <VWAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Species: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Accession: A37979; B37979
R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh Jacot Chem. 265, 19674-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix A;Reference number: A37979; MUID:91060568
                                                                                                                                                                                  A; Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1; C; Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin tF; 512-679/Domain: von Willebrand factor type A repeat homology <VWA1>F; 754-793/Domain: fibronectin type II repeat homology <2F1>FF1201-1244/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 CYGGFVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVFKNEVLRFVREFV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYFILDKSGSVLHH--WNEIYYFVEQLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   649 TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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                                                                                                                                                                                                                                                                                                                                                                                                        7.4%; Score 128; DB 2; Length 3051; 27.1%; Pred. No. 0.15; ive 31; Mismatches 75; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;227-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology
F;76,344/Einding site: carbohydrate (Asn) (covalent) #status pr
F;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                A;Molecule type: DNA
A;Residues: 1-3051 <SMI>
A;Crost-references: EMBL:Z30423; NID:g458479; PID:g458485
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.0%; Score 120.5; DB 2;
25.3%; Pred. No. 0.055;
tive 37; Mismatches 95;
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A;Cross-references: GDB:127280; OMIM:115437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cartilage matrix protein precursor - human
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nes 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 25.3
Matches 60; Conservative
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A; Accession: B37979
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A; Residues: 1-496 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 CYGGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A37979
                                A; Accession: S42373
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A: Superfamily: complement alternate pathway
A: Pathway: complement alternate pathway
C; Superfamily: complement C2; complement factor H repeat homology; trypsin homology;
C; Superfamily: complement alternate pathway; duplication; glycoprotein; hyd
C; Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hyd
C; Keywords: acute phase; complement factor B *fratus experimental <MAT>
F; 26.764/Product: complement factor B *fragment *fstatus experimental <BAF>
F; 36.98/Pomain: complement factor H repeat homology <FH3>
F; 163.218/Domain: complement factor H repeat homology <FH3>
F; 165.218/Domain: complement factor H repeat homology <FH3>
F; 268.764/Product: C3/C5 convertase Bb fragment *status experimental <BBF>
F; 268.764/Product: C3/C5 convertase Bb fragment *status experimental <BBF>
F; 37.76, 62.98, 103.145, 131.128, 165.205, 191.218, 478-366, 511.227, 599.615, 656.682, 695.725
F; 37.76, 62.98, 103.145, 131.128, 165.205, 191.218, 478-366, 511.227, 599.615, 656.682, 695.725
F; 329.260/Cleavage site: Arg-Lys (complement factor D) *status experimental F; 226, 576, 699/Active site: His, Asp, Ser *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alph
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243 EGVDAEDGHGPGEQOKRKIVLDPSGSMNIYLVLDGSDSIGASNFTGAKKCLVNLIEKVAS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 KFISPQLRMSFIVFSTRGTTLMKLTE----DREQIRQGLEEL----QKVLPGGDTYMHEG 123
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356 -KKALQAVYSAMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.6%; Score 113.5; Di
19.6%; Pred. No. 0.37;
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Best Local Similarity 19.6
Matches 66; Conservative
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A.Status: mRNA
A.Molecule type: mRNA
A.Residues: 16-225, F', 227-259 <MOR>
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
A.Title: Human complement factor B: functional properties of a recombinant zymogen of th
A.Reference number: 154409; MUID:94041399
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A; Title: Internal homologies of the Ba fragment from human complement component factor A; Reference number: A44628; MUID:84158524
                                                                                                                                                                                                                        a class
                                                                                                             A;Cross-references: EMBL:X72875; NID:9297568; PIDN:CAA51389.1; PID:9297569 R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R. Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982 A;Title: Isolation of CDNA clones for the human complement protein factor B, A;Reference number: A44622; MUID:83039428
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A; Residues: 270-329 <NIE>
                                         A; Accession: S34075
A; Molecule type: mRNA
A; Residues: 1-764 <MEJ>
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C; Function:
A; Description: structural component of extracellular polymer associated with anchorin C; Superfamily: unassigned collagens; animal Kunitz-type proteinase inhibitor homology C; Keywords: collad coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr F; 116/Domain: signal sequence #status predicted <SIG> F; 17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT> F; 17-253/Domain: aminor terminal nonhelical #status predicted <MAT> F; 17-253/Domain: uninor terminal nonhelical #status predicted <MAT> F; 21-31-316/Domain: the monoterminal nonhelical #status predicted <MAI> F; 31-316/Domain: the monoterminal nonhelical #status predicted <MAI> F; 31-316/Domain: fibronectin type III repeat homology <FN2> F; 368-583/Domain: fibronectin type III repeat homology <FN5> F; 568-583/Domain: fibronectin type III repeat homology <FN5> F; 568-583/Domain: fibronectin type III repeat homology <FN3> F; 568-583/Domain: fibronectin type III repeat homology <FN3> F; 568-582/Domain: fibronectin type III repeat homology <FN3> F; 568-582/Domain: fibronectin type III repeat homology <FN9> F; 568-1045/Domain: fibronectin type III repeat homology <FN9> F; 568-1045/Domain: fibronectin type III repeat homology <FN9> F; 5118-1228/FR9jon: cell attachment (R-G-D) motif F; 118-1228/FR9jon: cell attachment (R-G-D) motif
     Complex: type VII collagen is probably a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:1334-1336/Region: cell attachment (R-G-D) motif
F:2008-2010/Region: cell attachment (R-G-D) motif
F:2553-2555/Region: cell attachment (R-G-D) motif
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Job time: 260 sec
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Matches 52; Conserv
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A;Nolecule type: mRNA
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A;Residuse: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A;Cross-references: GB:S51236; NID:3262308; PIDN:AAB24637.1; PID:g262309
B;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
A; Title: Chem. 254, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A;Reference number: A30296; MUID:89139437
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A; Residues: 815-892, E', 894-1439 < PAR>
A; Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A; Experimental source: keratinocyte
R; Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
A; Tivest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
A; Reference number: 156328; MUID:93107742
                                                                                                                                                                              C.Date: 04 NOV-1994 #sequence_revision 04-Nov-1994 #text_change 20-Sep-1999
C.Accession: A54849; PH0844; 516316; 156328; A30296; 184686
R.Christiano, A.M.; Greenspan, D.S.; Lee, S.; Ultto, J.
Blol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alphal(VII A;Reference number: A54849; MUID:94327588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528, 'C',
A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528, 'C',
A; Cross-references: DDBJ:D11152; DDBJ:D13694; NID:9453698; PIDN:BAA02853.1; PID:9453699
A; Experimental source: keratinocyte
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R; Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A; Title: Human type VII collagen: CDNA cloning and chromosomal mapping of the gene.
A; Reference number: S16316; MUID:91334380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --> Ser subs
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A;Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous A;Reference number: 148103; MUID:93271985
A;Accession: 184686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Wolecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
R;Greenspan, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently O-glycosylated.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 2395-2871, 'S., 2873-2944 <RE2>
A;Residues: 2395-2871, 'S., 2873-2944 <RE2>
A;Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
B;Christiano, A.M.; Rynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3540-3553, 1994
A;Tille: Dominant dystrophic epidermolysis bullosa: identification of a Gly
A;Reference number: A55255; MUID:94224777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; cross-references: GB:L02870; NID:9987124; PIDN:AAA75438.1; PID:9987125 R: Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A; Ittle: Molecular cloning and characterization of type VII collagen cDNA. A; Reference number: PHO844; MUID:92231902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: not compared with conceptual translation
A54849

Collagen alpha 1(VII) chain precursor - human
N,Alternate names: procollagen alpha 1(VII) chain
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:COL7A1; EBR1; EBD1; EB
A;Cross-references: GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-2944 <CHR>
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F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2784-2924/Domain: animal Kuntze-type proteinase inhibitor homology GBIP-
F;287-2929/Domain: animal Kuntze-type proteinase inhibitor homology GBIP-
F;337,786.1109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status ex
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Modified site: carbohydrate (Lys) (covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 TEDREQIRQGLEELQKVLPGGDTYMHEGFBRASEQIYYENRQGYRTASVIIALTDGELHE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2944;
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                                                                                                                                                                                                                                                                                                                        6.5%; Score 111.5; DB 2; 24.1%; Pred. No. 3.3; tive 42; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                                                   52; Conservative
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Human immune/haema

Murine

Mouse alpha-d subu Mouse beta 2 integ Mouse beta a integ Mouse alpha d poly Mouse alpha-d prote Mouse alpha-d subu Mouse alpha-d subu Mouse alpha-d #2. Mouse alpha d #2. Mouse alpha d poly Mouse alpha d poly Mouse alpha d poly Mouse alpha d prote Mouse alpha d prote Mouse alpha d prote Mouse alpha-d prote Mouse alpha-d prote Rat alpha-d protein Rat alpha-d partia Rat alpha-d subuni Human beta-2 integri Human alpha-d deri Rat alpha-d deri Rat alpha-d af integri

OM protein

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Sequence:

Searched:

Database

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TANGO: 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prognosis; prophylatic; therapeutic; human.
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                        AAW23049
AAW72837
AAW72824
AAW72825
AAB18448
AAB18460
AAB18459
                               AAB01428
AAM84307
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AAW65101
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AAR78169
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB01422 standard; Protein; 333 AA.
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  99WO-US31025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
 WPI; 2000-465743/40.
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A human TANGO 216
A human TANGO 216
Human novel extrac
A murine TANGO 216
                                                                                                                                                                                                                                                                                                             1: /SIDSI/gcgdata/hold geneseq/geneseqp-embl/AA1980 DAT:*
2: /SIDSI/gcgdata/hold geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold geneseq/geneseqp-embl/AA1982.DAT:*
5: /SIDSI/gcgdata/hold geneseq/geneseqp-embl/AA1983.DAT:*
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7: /SIDSI/gcgdata/hold geneseq/geneseqp-embl/AA1986.DAT:*
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10: /SIDSI/gcgdata/hold geneseq/geneseqp-embl/AA1989.DAT:*
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Human protein sequ
A human TANGO 216
                                                                                 (without alignments)
310.481 Million cell updates/sec
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Human gene 4 encod
Human gene 4 encod
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                                                                                                                                     1 MATAERRALGIGFQWLSLAT......TTHCSLHKIASGPTTAACME 333
                                                                        ; Search time 119.13 Seconds
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                      Compugen Ltd
                                                                                                                                                                                                            hits satisfying chosen parameters:
          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                       747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft especials controlled actachilis, posniasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, tame's disease, osteoarthritis, Lyme's disease, cacheria and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lipus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in parmacogenomics and for monitoring clinical trials. TANGO plarmacogenomics and for monitoring clinical trials. TANGO colypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a colypeptides are solitable for the prophylactic and therapeutic disorder associated with aberrant TANGO expression. A wide range
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                Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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100.0%; Pred. No. 5e-
:ive 0; Mismatches
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                                                                                                                Claim 8; Fig 4; 209pp; English.
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Best Local Similarity
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N-PSDB; AAA47455
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AAD05300-AAD05379 represent CDNAs corresponding to 28 human secreted protein genes, and AAE01544 represent human secreted protein fragments or variants. AAE01514-AAE01544 represent human secreted protein fragments or variants. CAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the presence of amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the new proteins of the diagnosis or treatment of and include developing products for the diagnosis or treatment of and include developing products for the diagnosis or treatment of an include developing products for the diagnosis or treatment of an include developing products (e.g., rheumatoid arthritis), inflammation, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, architestinal disorders, populasis), sepsis, diabetes, atherosclerosis, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, skin disorders, prognancy-related disorders, enditing and epithelial cell proliferation, to prevent skin adiom coll continue of primary tissues, to regenerate tissues, to identify their culture of primary tissues, to regenerate tissues, to identify their culture of primary tissues, to regenerate tissues, condacting and editive or preservative to modify storage properties.

C alleviating symptoms associated with the disorders mentioned above, and im diagnostic immunosasays e.g., radioimmunosasay or enzyme limman immunosasay or enzyme limman immunosasay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19.
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                                                                                                                                                                                                                                                          /note= "Mature human secreted protein"
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100.0%; Pred. No. 2.1e-168;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 485-486; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM, Komatsoulis GA, Moore PA,
                                                                                                                                                                                                          1..27
/label= Signal_peptide
28..403
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1999; 99US-0163581.
30-JUN-2000; 2000US-0215133.
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N-PSDB; AAD05303.
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Matches 318; Conserv
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                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                        Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; Schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; predated disorder; endocrine disorder; predated disorder; cellated disorder; cellated disorder; cellated disorder; cellated disorder; cellated disorder; cellated disorder; difection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                            EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                        HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                  VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
                                                                                                                                                                                                                                                                                                         Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mature human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                     binding partner identification; chromosome 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by KTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Encoded by WGC"
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/note= "Encoded
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/note= "Encoded
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Abd05300-Abd05379 represent cDNAs corresponding to 28 human secreted cordein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions and alternative disorders, diseases of the immune system, abnormalities, haematopoietic disorders, diseases of the immune system, alleryies, neurological disorders, schizophrenia, asthma, alleryies, neurological disorders, schizophrenia, asthma, and infections. The proteins can also be used to aid wound the strongers and infections. The proteins can also be used to aid wound control printing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting colluture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in removers and in cell proliferation. The motein of the invention can be used in diagnostic immunosassay e.g., radioimmunosassay or enzyme linked in invention.

Antibodies specific for a protein of the invention epercent a human control of the invention.
                                                                                                                                                                                                                                New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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Pred. No. 7.3e-168;
0; Mismatches 1;
                                                                   Birse CE,
                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 505-506; 562pp; English.
                                                                       Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.1%;
Best Local Similarity 99.7%;
Matches 317; Conservative 0
(HUMA-) HUMAN GENOME SCI INC.
                                                                       Komatsoulis GA,
                                                                                                                                       2001-308778/32,
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                        HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                      1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
                                                                                      KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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Otsuki
Score 1392; DB 22; J
Pred. No. 5.9e-141;
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A, Nagai K,
                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:11706.
                                                                                                                                                                                                                                                                                                               241 VRGNGFRHARNVDRVLCSFKINDSVTLNE 269
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Sugiyama T, Wakamatsu
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                     80.6%;
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                                                  Conservative
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                         Query Match
Best Local Similarity
Matches 267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful immunosuppressant and cytostatic activity. The polypucleotides are useful in gene thereapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemotactic/chemokinetic activity, haemotactic/chemokinetic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemothic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemothic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
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Zhang J;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 2121; 10078pp; English.
                                                                                                                                        AAM38976 standard; Protein; 297 AA.
                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 2121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0590042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653451.
19-CCT-2000; 2000US-063036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263.
                                                   301 dglsfisssviitthcs 318
                                                                                                                                                                                                     (first entry)
                                     DGLSFISSSVIITTHCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
N-PSDB; AAI58132.
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03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
29-NOV-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
                                                                                                                                                                                                     22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang J, W
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                    leukaemia.
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                                                                                                                                                                          AAM38976;
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                                                                                                                              AAM38976
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                                                    the 5'-end sequence's end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13628 and AAH13631 to AAH13612 represent human cDNA sequences; AAH03166 to AAH13622 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 259
                                                                                                                                                                                                                                                                                                                                                                                                                            80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                Score 966; DB 22;
Pred. No. 2.5e-95;
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                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB18456 standard; Protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                55.9%;
98.9%;
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                                                                                                                                                                                                                                                        the present invention.
                                                                                                                                                                                                                                                                                                                                                                                        Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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181 kindsvtlsk 190
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                                                                                                                                                                                                                                                                                          218 AA;
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                                                                                                                                                                                                                                                                                            Sequence
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cescribes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cellular proliferation, modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation of isorders, such as cancer, and thematopoietic associated diseases and disorders, such as cancer, and hematopoietic associated diseases and disorders, spleen associated diseases and disorders, spleen associated associated diseases and disorders, spleen associated associated diseases, modulate the proliferation, differentiation, asthma and bronchlectasis, intestinal disorders, spleen associated as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral ocdema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bydrocephalus and encephalitis, and treat hepatic disorders.

Correlal and viral meningitis, alzhalmer's Disease, prain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Correlation of bone and cartilage associated of the sease, multiple sclerosis, brain cancers, corebrain cancers, and created of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core of the core
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
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                                                                                            Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
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51.3%; Pred. No. 4.2e-77;
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                                                                                                                                                                                                       Disclosure; Page -; 175pp; English.
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301 ksvisgslivtatecs 316
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                                                                                                                                                      e.g. for treating cancer
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Best Local Similarity
                     2000-579269/54.
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N-PSDB; AAA75149.
                                                   WO200052022-A1
                                                            01-MAR-1999;
                      Homo sapiens
                                                      08-SEP-2000
                          Peptide
                                Protein
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TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; when willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; ocdema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; brain herniation; iatrogenic disease; inflammation; meningitis; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 488;
                                                                                                                                                                                                                                     Score 800.5; DB 21;
Pred. No. 5.4e-77;
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                                                                                                                                                                                                                                        46.3%; Scor.
51.3%; Pred. No. 5...
'... 56; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A human TANGO 216 polypeptide clone.
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                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                        488 AA;
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                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 162;
                                                                                                                                               disorders.
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                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                 Query Match
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                              The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular contribution and/or modulate cellular adhesion, modulate estracellular matrix structuring, factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, disorders, such as cancer, modulate the proliferation, differentiation, disorders, such as cancer, modulate the proliferation, differentiation, disorders, such as cancer, undonear in the bone marrow, and leukocytes, and/or function of cells that appear in the bone marrow, and leukocytes, creat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, plumonary congestion or cedema, emphysema, chronic bronchitis, bronchial asthma and bronchictasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders such as ischemic heart disease, or cells and to treat bone and/or cartilage associated diseases or
                                                                                                                 TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; higheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human and murine secreted proteins designated TANGO 216, 261, 266 and 267 useful as modulating agents of ceilular processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44..213
/note= "von Willebrand factor A domain"
                                                                                   Amino acid sequence of human TANGO 216 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser CC;
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342..488
/note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Fig 1A-C; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0122458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2000; 2000WO-US05226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262, 266 and 267 usetul a
e.g. for treating cancer
                                             15-JAN-2001 (first entry)
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(first entry)

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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                   TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                      A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2000; 2000WO-US05226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnes TM, Holtzman DA,
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                                                                                                                                                                                                                                                                                                                           Homo sapiens.
15-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-2000.
describes TANGO 266, TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 261 polypeptides can be used to endulate cellular adhesion. Modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular and acancer, modulate cell adhesion in proliferation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoletic associated diseases and disorders, atelectasis, and hematopoletic associated diseases and disorders, spleen associated diseases. Modulate renal disorders, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral ocedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, cerebral cerebral cerebral cellular.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 ENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes,
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Pred. No. 8.9e-77;
5; Mismatches 87; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     created using information provided.
                                                                                                                                                                      Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
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52.18;
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                                                                                                                         for treating cancer
                  2000-579269/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 AA;
                                        N-PSDB; AAA75157
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                                                                                                                              e.g.
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Fraser CC;

Sharp JD,

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ABB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 clular differentiation and/or modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The proteins can be used to creat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion in proliferation, and/or function of cells modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, apleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral ocedema, hydrocephalus, brain hermiations, latrogenic disease, inflammations, latrogenic disease, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
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50.9%; Pred. No. 1.1e-76;
ive 57; Mismatches 95
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12-SEP-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
             14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
22-AUG-2000;
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01-SEP-2000;
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Human; secreted extracellular matrix protein; immunomodulatory; Anti-HTV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzbelmens; immuned/autoimmune disease; HTV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; sezary syndrome; Gaucher's disease; neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; parkinson's disease; cardiovascular disorder; cardiac arreat; tachycardia; angina; infection; corneal infections; cardiac all munogen; gene therapy; antisense; food additive.
                                                                                   YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
                 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
                                                                                                           243 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG
                                                                                                                                                                                                                                                      Human novel extracellular matrix protein, Seq ID No 312.
                                                                                                                                                                                                        AAU19662 standard; Protein; 587 AA
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2000US-0180628.
2000US-0184644.
2000US-0189874.
2000US-0199076.
2000US-0199774.
2000US-0209467.
2000US-0209467.
2000US-0215135.
2000US-0215135.
2000US-0217487.
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20000S - 0224518.
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20000S - 0225213.
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24-FEB-2000; 2
16-MAR-2000; 2
11-MAR-2000; 2
11-MAR-2000; 2
11-MAR-2000; 2
19-MAY-2000; 2
19-MAY-2000; 2
28-JUN-2000; 2
30-JUN-2000; 2
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
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14 - SEP - ZOUO; ZOUOUS - OZ32400.

14 - SEP - ZOUO; ZOUOUS - OZ32401.

14 - SEP - ZOUO; ZOUOUS - OZ33461.

14 - SEP - ZOUO; ZOUOUS - OZ33064.

14 - SEP - ZOUO; ZOUOUS - OZ33065.

15 - SEP - ZOUO; ZOUOUS - OZ34223.

21 - SEP - ZOUO; ZOUOUS - OZ34223.

25 - SEP - ZOUO; ZOUOUS - OZ34298.

25 - SEP - ZOUO; ZOUOUS - OZ34298.

26 - SEP - ZOUO; ZOUOUS - OZ34898.

27 - SEP - ZOUO; ZOUOUS - OZ34898.

28 - SEP - ZOUO; ZOUOUS - OZ34898.

29 - SEP - ZOUO; ZOUOUS - OZ36387.

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29 - SEP - ZOUO; ZOUOUS - OZ36387.

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20 - CCT - ZOUO; ZOUOUS - OZ36380.

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20 - CCT - ZOUO; ZOUOUS - OZ36393.

13 - CCT - ZOUO; ZOUOUS - OZ39933.

13 - CCT - ZOUO; ZOUOUS - OZ39933.

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2000US-0246523.
2000US-0246524.
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2000US-0241809.
2000US-0241826.
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2000US-0225270.
2000US-0225477.
2000US-0225757.
2000US-0225759.
2000US-0226759.
2000US-0226868.
2000US-0226868.
2000US-0228924.
2000US-0228924.
2000US-0229343.
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2000US-0230437.
2000US-0230438.
2000US-0231242.
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2000US-0232398
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2000US-0229509
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPS). The novel human secreted extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPS by binding with the cells own genes and preventing their expression. The polynucleotides may be as antigens to produce antibodies and to identify modulators used as antigens to produce antibodies and to identify modulators used as antigens to produce antibodies and to identify modulators antagonists and antagonists of the SPS. The anti-(SP) antibodies and antagonists and actecting the presence of SPS in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers
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Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                               347
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                                                                                                                                                                                         74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYY 133
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                                                                                                     Score 785.5; DB Pred. No. 3e-75;
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Best Local Similarity 51.8%; Pred: No. 3e-7;
Matches 158; Conservative 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A murine TANGO 216 polypeptide clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAB18448 standard; Protein; 487 AA.
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                         Disclosure; Page -; 175pp; English.
Novel human and murine secreted
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| ndgksavsrsltitatect 316
                                                                                                                                                                                                                        44.78;
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      262, 266 and 267 useful as e.g. for treating cancer -
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                                                                                                                                                                                                     Sequence
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15-JAN-2001

AAB18448;

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The present sequence represents a murine TANGO 216 polypeptide. The control also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular modulate cellular adhesion, modulate cellular adhesion. The proteins can be used to treat any von Willebrand cellular adhesion. The proteins can be used to treat any von Willebrand cellular adhesion, and cell trafficking and/or matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, modulate extracellular matrix structuring, cellular interactions, modulate cell adhesion in proliferation, disporders, such as cancer, modulate the proliferation, differentiation, differentiation, disporders, and leukocytes, creat bone marrow, blood and hematopoietic associated diseases and chronic bronchitis, bronchial asthma and bronchiectasis, intestinal chronic bronchitis, bronchial asthma and bronchiectasis, intestinal conforcers, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders as ischemic heart disease, modulate the cardiovascular disorders as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated with the consider of the pang also be used to treat disorders associated with the consider of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of
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                  cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; cedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spheen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; harin herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "cytoplasmic uc....
/note= "cytoplasmic uc....
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.+e= "transnmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/note=
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N-PSDB; AAA75150.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                  AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 257. The TANGO CCC describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO CCC describes TANGO 266, TANGO 262, and TANGO 267. The TANGO CCC cellular differentiation modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, composition in proliferation, modulate cellular interactions, and cell trafficking and/or migration, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoletic associated diseases and disorders, atelectasis, confidential disorders, spleen associated diseases and disorders, spleen associated diseases modulate the proliferation, differentiation, as ischemic and cartilage cells and cortained as also be used to creat disorders associated with the ovaries, and cerebral ocdema, treat disorders associated with the ovaries, and cerebral ocdema, treat disorders associated with the ovaries, and cerebral ocdema, treat disorders associated with the ovaries, and cerebral ocdema, they disease, milipple sclerosis, brain meningits, Alzheimer's Disease, cerebral corters, parkinson's disease, multiple sclerosis, brain cortained constant hepatic disorders.

Contect the present sequence does not appear in the specification; it was considered with the ovaries of the particular of the constant of the present sequence does not appear in the specification; it was
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                     nurine secreted proteins designated TANGO 216, 261, useful as modulating agents of cellular processes,
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e.g. for treating cancer
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Best Local Similarity
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cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor associated disorder; cell trafficking; cancer;
hematopoietic associated disorder; cell trafficking; cancer;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; latrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                       60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY 119
                                                                                                                                    MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG 179
                                                                                                                                                                          VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV 239
                                                                                                                                                                                                                    240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                                                                                                                                                                                                                                                                      238 vltgravtsishdgsvlctftanstytksekpvsiqpssilcpapvlnkdgetlevsisy 297
                                                             Gaps
                                                                               1 MATAERRALGIGFQWLSLATLVLICAGOGG-RREDGGPACYGGFDLYFILDKSGSVLHHW 59
                                                                                          Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                             4;
                                      Length 487;
                                     Score 771; DB 21; Length 4
Pred. No. 8.1e-74;
3; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser CC;
                                                                                                                                                                                                                                                                                                                                                                                                                             A murine TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharp JD,
                                                           53;
                                                                                                                                                                                                                                                                                                                                                                 AAB18460 standard; Protein; 487
                                      44.68;
                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                           NDGLSFISSSVIITTTHCS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2000; 2000WO-US05226.
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holtzman
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                                                 Similarity
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        487
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                                                            Matches 158;
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        Sequence
                                       Query Match
Best Local (
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describes TANGO 266, TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO 260 cellular be used to modulate cellular proliferation, modulate cellular adhesion, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation in proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, understooletic associated diseases and disorders, spleen associated associated diseases and disorders, spleen associated consideration of pronchiectasis, intestinal disorders, spleen associated as such as isohemic heart disease, modulate trenal disorders, treat cardiovascular disorders such as isohemic heart disease, modulate the proliferation, differentiation, and or inteat bone and/or modulate the proliferation of bone and cartilage cells and to treat bone and/or modulate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimmer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 MHEGFERASEQIYYENRQGYRTASVIIALIDGELHEDLFFYSEREANRSRDLGAIVYCVG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.6%; Score 770; DB 21; Length 487; 49.5%; Pred. No. 1e-73; ive 53; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A murine TANGO 216 polypeptide clone.
Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB18459 standard; Protein; 487 AA.
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 267, and TANGO 267. The TANGO 267 the TANGO 267. The TANGO 267 the TANGO 267. The TANGO 267 the TANGO 267 the tangent of the collular descration, modulate cellular differentiation and/or modulate cellular adhesion. The disorder, regulate extracellular matrix structuring, cellular adhesion, cellulate cell rafficking and/or migration, modulate cellular interactions, and cell trafficking and/or migration, modulate cellular interactions, combilate the proliferation in proliferative disorders, such as cancer, combilate the proliferation, differentiation, and/or function of cells modulate the proliferation of disorders, treat bone marrow, blood that appear in the bone marrow, and leukocytes, treat bone marrow, blood such and bronchietated diseases and disorders, atelectasis, pronchial combined trains, and isorders, spleen associated as associated disorders, reat cardiovascular disorders such disorders associated disorders, treat cardiovascular disorders and/or function of bone and cartilage cells and to teat bone and/or cartilage associated with the ovaries, and cerebral oceana, cartilage cells and to disease, inflammations, hydrocephalus, brain heniations, latrogenic disease, cerebral concephalus and encephalitis, and treat hepatic disorders. In the procession of concerns and core and the procession of the propertication; it was notes and very may also be used to concerns and viral meningitis, and treat hepatic disorders. In the procession of core and meningitis, and treat hepatic disorders. In the specification; it was notes and viral meningitis, and treat hepatic disorders.
           hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 mvagrsrarspg-swlfpglwllavggpgsllqaqeqpsckkafdlyfvldksgsvannw 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
cell trafficking; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.4%; Score 768; DB 21;
49.2%; Pred. No. 1.7e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sharp JD, Fraser CC;
       Willebrand factor-associated disorder;
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157; Conservative
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Gaps

120 MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG 179

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agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chod colitis, Crohn's disease, content and autoimmune disease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic diseases e.g. myasthemia gravis, autoimmune diabetes and systemic clasease e.g. myasthemia gravis, propositis themselves. Partial transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in parmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a methods for treating a subject at risk of a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TANGO; 128: 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host disease; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia cancer; liver disease; hodyfin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse.
                                                                                                                            240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                                                     180 VKDFNETQLARIADSKDHVFPVNDGFQALOGIIHSILKKSCIEILAAEPSTICAGESFQV 239
                                                                                                                                                  Nucleic acids encoding TANGO polypeptides are useful as modulating
                                                                           AAB01428 standard; Protein; 381 AA.
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                                                                                                                                                                                                                   300 NDGLSFISSSVIITTHCS 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine TANGO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200039284-A1.
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of cellular disorders can be treated.

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187 OLARIADSKDHVPPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 246
                                                                                                                                                                                           247 RHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFI 306
                                                                                                       0; Gaps
                                                                        Query Match
38.7%; Score 669; DB 21; Length 381;
Best Local Similarity 99.2%; Pred. No. 5.2e-63;
Matches 131; Conservative 1; Mismatches 0; Indels
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124 SSSVIITTTHCS 318
                              Sequence 381 AA;
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Search completed: August 9, 2002, 10:32:14 Job time: 133 sec

(Orasu) XNAJB 39A9 21HT

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:35:55 ; Search time 98.32 Seconds (without alignments) 1005.580 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-970-076-6 3025 1 MATAERRALGIGFQWLSLAT......QAPPPNRAPPPSRPPRPSV 564

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

528882 seqs, 175299045 residues Searched:

528882 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 187, App	232,	1823,	194,	301,	4, Ap	18	~	Sequence 24, Appl	20,	26,	22,	14,	16,	10,	12,	2639		Sequence 10, Appl	œ	312					Sequence 9405, Ap
	ID	PCT-US02-08253-187	PCT-US02-08253-232	US-60-389-987-1823.	PCT-US02-08253-194	PCT-US02-08253-301	US-10-038-307-4	US-10-038-307-18	US-10-038-307-2	US-10-038-307-24	US-10-038-307-20	US-10-038-307-26	US-10-038-307-22	US-10-038-307-14	US-10-038-307-16	US-10-038-307-10	US-10-038-307-12	US-10-104-047-2639	US-10-038-307-6	US-60-373-595-10	US-10-038-307-8	US-10-125-540-312	US-09-629-469A-11706	US-10-047-542-99	US-09-935-625-9406	US-09-935-625-26246	US-09-935-625-9405
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	Query Match Length DB	564	564	564	562	562	381	551	333	345	564	328	342	543	543	543	534	488	488	488	487	587	218	538	1589	1589	1615
æ	Query	100.0	100.0	100.0	95.9	95.9	66.7	54.9	54.5	54.5	54.5	54.1	54.0	53.9	53.9	53.5	49.2	46.8	46.7	46.7	46.2	39.9	31.9	29.9	7.0	7.0	7.0
	Score	3025	3025	3025	2901	2901	2017	1991	1649	1649	1649	1636	1634.5	1629	1629	1619	1488	1416.5	1411.5	1411.5	1396.5	1206.5	996	903	211	211	211
	Result No.	-	7	m	4	S	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56

Sequence 26245, A Sequence 9404, Ap	Sequence 26244, A	Sequence 9383, Ap	Sequence 17852, A	Sequence 9382, Ap	Sequence 17851, A	Sequence 9381, Ap	Seguence 17850, A	Sequence 900, App	Sequence 5343, Ap	Sequence 8099, Ap	Sequence 25320, A	Sequence 899, App	Sequence 5342, Ap	Sequence 8098, Ap	Sequence 25319, A	Sequence 898, App	Sequence 5341, Ap
US-09-935-625-26245 US-09-935-625-9404	-935-625-	US-09-935-625-9383	625-	US-09-935-625-9382	US-09-935-625-17851	US-09-935-625-9381	US-09-935-625-17850	US-09-935-625-900	US-09-935-625-5343	US-09-935-625-8099	US-09-935-625-25320	US-09-935-625-899	US-09-935-625-5342	US-09-935-625-8098	US-09-935-625-25319	US-09-935-625-898	US-09-935-625-5341
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211	211	199.5	199.5	199.5	199.5	199.5	199.5	194	194	194	194	194	194	194	194	194	194
27	56	30	31	32	33	34	32	36	37	38	38	40	41	43	43	44	45

ALIGNMENTS

RESULT	T
PCT-U	PCT-0502-08253-187
Sed	Sequence 18/, Application PC/TUSUZU8253
APP.	ENERAL INFORMATION: APPLICANT: Carson-Walter, Fleanor
, AP	
; A P	
; A P	ANT: Kinzler, Kenneth
. III	TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
	FILE REFERENCE: IIO/.OOI/9 CHRRENT ADDITCATION NIMBER: DCT/US02/08253
G	CURRENT FILING DATE: 2002-04-10
, PR	
PR	PRIOR FILING DATE: 2001-04-11
B	FILING DATE: 2001-08
DN	OF SEQ ID NOS: 359
os :	SOFTWARE: FastSEQ for Windows Version 4.0
SEO :	
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PCT-U	CONSTALLSM: HOMO SAPIEUS PCT-US02-08253-187
Query	Match 100.0%;
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ò	61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
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qq	61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
Qy	121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
qq	121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
οy	181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
qq	181 KDENETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
δλ	241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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ESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKM
                                              PEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGR
                                                                                    CINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPPSAPTPPIPSPSTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 564;
                                                                                                                                                                                                                   Sequence 23. Application PC/TUS0208253
; Sequence 23. Application.
; Sequence 23. Application.
; General information:
    Applicant: Carson-Walter, Eleanor
    Applicant: Carson-Walter, Eleanor
    Applicant: Occis, Brad
    Applicant: Vogelstein, Bert
    Applicant: Vogelstein, Bert
    Applicant: Winaler, Kenneth
    TILE REPERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: PCT/US02/08253
; CURRENT FILING DATE: 2002-04-10
    PRIOR FILING DATE: 2000-04-10
    PRIOR FILING DATE: 2001-04-11
    PRIOR FILING DATE: 2001-04-11
    PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SEQ ID NOS: 359
; SEQ ID NOS: 359
; SEQ ID NOS: 359
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                                                                                                                                                         PPPPQAPPPNRAPPPSRPPRPSV 564
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PCT-US02-08253-232
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ENGTH: 564
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKÞFSVEDTYLLCPAFILKEVGMKAALQVSMN 300
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                 PEQEYEFPEPRILINNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGR 480
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ESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKM
                                                                                                                                                                                                                                                                                                                                          US-0U-389-98/-1863
Sequence 1823, Application US/60389987
Sequence 1823, Application US/60389987
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fang, Bin D.
APPLICANT: Gloson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660084 465P2
CURRENT FILING DATE: 2002-06-17
CURRENT FILING DATE: 2002-06-17
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 3e-176;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 564; Conservative
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; ORGANISM: Homo sapiens
US-60-389-987-1823
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ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH 248
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GENERAL INFORMATION:

APPLICANT: Carson-Walter, Eleanor

APPLICANT: Carson-Walter, Eleanor

APPLICANT: St. Carix, Brad

APPLICANT: Vogelstein, Bert

APPLICANT: Wogelstein, Bert

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: PCT/USO2/08253

CURRENT APPLICATION NUMBER: 60/282,850

PRIOR PAPLICATION NUMBER: 60/282,850

PRIOR PELING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 60/308,829

PRIOR PILING DATE: 2001-08-01

WUMBER OF SED ID NOS: 359

SOFTWARE: FastSEQ for Windows Version 4.0
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96.8%; Pred. No. 1e-168;
ive 7; Mismatches 1
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538; Conserv
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PCT-US02-08253-301
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PCT-US02-08253-301
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ESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKM 420
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APPLICANT: Carson-Walter, Brad
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kincler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPRENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/USO2/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PAPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
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Pred. No. 1e-168;
7; Mismatches 11;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                           Sequence 194, Application PC/TUS0208253 GENERAL INFORMATION:
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Best Local Similarity 96.8%;
Matches 538; Conservative
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PCT-US02-08253-194
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Query Match
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Matches 318; C
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LENGTH: 333
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Number 18, Application US/10038307
Sequence 18, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
APPLICANT: The PERENCE: 7853-253-999
                                                                                                                                                        APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 381
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
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Best Local Similarity
Matches 371; Conserv
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US-10-038-307-4
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-10-038-307-4
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US-10-038-307-2

Sequence 2, Application US/10038307

Sequence 2, Application US/10038307

Sequence 2, Application US/10038307

Sequence 2, Application US/10038307

APPLICANT: Theresa L. O'KEEE

APPLICANT: Theresa L. O'KEEE

APPLICANT: Andth J. HEALEY

APPLICANT: Andth J. HEALEY

TILLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

TILLE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ 1D NOS: 26

SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 7.5e-93;
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100.0%; Pred. No. 2.5e-93;
Live 0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 320; Conservative
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US-10-038-307-2
                                                                                   TYPE: PRT ORGANISM: Homo sapiens US-10-038-307-18
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LENGTH: 328
TYPE: PRT
CRGANISM: Homo sapiens
US-10-038-307-26
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Best Local Similarity
Matches 316; Conserv
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                   VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                    Compositions and Methods
                                                                 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
 HEGFERASEQ1YYENRQGYRTASV11ALTDGELHEDLFFYSEREANRSRDLGA1VYCVGV
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100.0%; Pred. No. 7.8e-93;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
ITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-223-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEO ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LEAGURE PRT
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Best Local Similarity 100.
Matches 318; Conservative
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US-10-038-307-24
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US-10-038-307-24
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APPLICANT: Engin OZKAYNAK
TOTALE APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
TITLE OF INVENTION: Tango 197
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 564
TYPE: PRT
TYPE: PRT
CORCANISM: Homo sapiens
US-10-038-307-20
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APPLICANT: Theresa L. O'KEFF
APPLICANT: Theresa L. O'KEFF
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 4.6e-92;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                54.5%; Score 1649; DB 6;
100.0%; Pred. No. 1.4e-92;
Live 0; Mismatches 0;
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Matches 318; Conservative
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Compositions and Methods

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KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.9%; Score 1629; DB 6; Length 543; 98.8%; Pred. No. 2.2e-91; ive 0; Mismatches 2; Indels ::
Sequence 14, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Com
TITLE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 16, Application US/10038307; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGLSFISSSVIITTTHCSDGS 321
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98.8%;
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Best Local Similarity 98.8
Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.9
Best Local Similarity 98.8
Matches 317; Conservative
                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-038-307-14
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US-10-038-307-16
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                                                                                                                                                                                                                                      VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                    HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                         KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                 Gaps
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                                                                                                                                                                                     1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGP------ACYGGFDLYFILDK
               EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/10038307;
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Theresa U. O'KEEFE
APPLICANT: The DOZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Com
TITLE OF INVENTION: Tango 197 and Tango 216 Com
TITLE OF INVENTION: 283-253-999
CURRENT APPLICATION UNBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 22
LENGTH: 342
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                                                                                                                                                                                                                                                                                                                                          DGLSFISSSVIITTTH 316
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US-10-038-307-22
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Matches 318; Conserv
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US-10-038-307-22
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US-10-038-307-14
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Query Match

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Gaps
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
TITLE COF INVENTION: Tango 197 and Tango 216 Compositions and 1
FILE REPERENCE: 7853-223-999
CURRENT FILING DATE: 2002-06-28
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEC ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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2;
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Pred. No. 2.2e-9
0; Mismatches
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Sequence 10, Application US/10038307

GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 543
TYPE: PRT
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                                                     61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                   HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                             181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                         241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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Pred. No. 8.8e-91;
0; Mismatches 3;
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Best Local Similarity 98.4
Matches 316; Conservative
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Search completed: August 9, 2002, 10:35:57

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OM protein - protein search, using sw model

August 9, 2002, 10:44:30; Search time 507.33 Seconds Run on:

(without alignments)
391.298 Million cell updates/sec

3025 1 MATAERRALGIGFÜWLSLAT......QAPPFNRAPPFSRPPRPSV 564 9-940-046-60-sn Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 3502263 seqs, 351980561 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

1: /cgn2_6/ptodate/2/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodate/2/paa/USO6_COMB.pep:*

4: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

5: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

6: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

7: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

8: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

9: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

10: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

11: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

12: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

13: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

14: /cgn2_6/ptodate/2/paa/USO8_COMB.pep:*

15: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

16: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

17: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

18: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

17: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

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18: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

19: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

20: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

21: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

22: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

23: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

24: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

25: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

26: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

27: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

28: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

28: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

28: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 187, App	Sequence 232, App	Sequence 6. Appli	Sequence 194, App	Sequence 301, App	Sequence 57, Appl	Sequence 57, Appl
SUMMARIES			ID	US-09-918-715-187	US-09-918-715-232	0-920-026-60-SD	US-09-918-715-194	US-09-918-715-301	PCT-US99-31025-57	US-09-471-179-57
			В	23	23	23	23	23	_	18
			ore Match Length DB ID	564	564	564	562	562	381	381
	æ	Query	Match	100.0	100.0	100.0	95.9	95.9	66.7	66.7
			Score	3025	3025	3025	2901	2901	2017	2017
		Result	No.	-	7	٣	4	S	9	7

Sequence 24, Appl Sequence 2, Appl1 Sequence 621, Appl Sequence 621, Appl Sequence 621, Appl Sequence 620, Appl Sequence 9, Appl Sequence 9, Appl Sequence 9, Appl Sequence 9, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 30, Appl Sequence 30, Appl Sequence 51, Appl Sequence 107, Appl Seque	equence 2 equence 2 equence 2
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ALIGNMENTS

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Sequence 187, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
TITLE OF INVENTYON: ENDOTHELIAL
TITLE OF INVENTYON: ENDOTHELIAL
CURRENT FILLIGO DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 05/22/599
PRIOR PILING DATE: 2000-08-02
PRIOR PAPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PILING DATE: 2000-08-12
PRIOR PPLICATION NUMBER: 60/224,360
PRIOR PPLICATION NUMBER: 60/224,360
PRIOR PPLICATION NUMBER: 60/224,360
PRIOR PPLICATION NUMBER: 60/282,850
PRIOR PPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2000-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 187
LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-918-715-187
US-09-918-715-187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Gaps ö Length 564; Indels Ouery Match 100.0%; Score 3025; DB 23; Best Local Similarity 100.0%; Pred. No. 1.4e-192; Matches 564; Conservative 0; Mismatches 0; I

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MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
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; Pred. No. 1.4e-192;
0; Mismatches 0; I
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Sequence 232, Application:
GENERAL INFORMATION:
APPLICANT: Brack St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATT
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: 06/022,599
PRIOR APPLICATION NUMBER: 06/224,599
PRIOR APPLICATION NUMBER: 06/224,360
PRIOR APPLICATION NUMBER: 06/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SEQ ID NO 232
LENGTH: FastSEQ for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
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Best Local Similarity 100.0%;
Matches 564; Conservative 0;
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US-09-918-715-232
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US-09-918-715-232
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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PEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGR
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100.0%; Pred. No. 1.4e-192;
.ive 0; Mismatches 0;
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APPLICANT: Young, John A.T.
APPLICANT: Collier, Rebert J.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
APPLICANT: Mogridge, Jeremy S.
FILLE REFERENCE: 960296.9776.
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
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Best Local Similarity 100.
Matches 564; Conservative
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                                          ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
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APPLICANT: BETG SL. CLIA.

APPLICANT: Kenneth Kinzler

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: US/09/918,715

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR FILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-04-11

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FREUENCY FOR WINDOWS VERSION 3.0

SEQ ID NO 301

LENGTH: 562
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ilarity 96.8%; Pred. No. 2.5e-184;
Conservative 7; Mismatches 11;
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Best Local Similarity
Matches 538; Conserv
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; ORGANISM: Mouse
US-09-918-715-301
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                  HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
                               KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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GENERAL INFORMATION:
APPLICANT: Beat Vogelstein
APPLICANT: Beat Vogelstein
TITLE OF INVATION: ENDOTHELIAL CELL EXPRESSION PAT':
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: 60/224,599
PRIOR APPLICATION NUMBER: 60/224,560
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SEOTTWARE: FESTSEQ FOI WINDOWS Version 3.0
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Pred. No. 2.5e-184;
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Matches 538; Conservative
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US-09-918-715-194
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LENGTH: 562
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APPLICANT: McCarthy, Sean A. TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-227-999 CURRENT PELLE RELECATION NUMBER: US/09/796,753 CURRENT FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
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US-09-796-753-24; Sequence 24, Application US/09796753; GENERAL INFORMATION:
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98.1%;
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Query Match
Best Local Similarity 98.1
Matches 371; Conservative
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Pred. No. 1e-125;
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ses 371; Conserv
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CRGANISM: Mouse
PCT-US99-31025-57
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                            VKNNQPAKYPLNNAYHTSSPPAPIYTPPPAPHCPPPPSAPTPPIPSPPSTLPPPQA 546
FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTR 303
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pred. No. 1e-125;
3; Mismatches 4; Indels 0
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GENERAL INFORMATION:
APPLICANT: HOLIZAMA, DOUGLAS
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS 1
FILE REPERBORS: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
WINDOW OF SETTING DATE: 1998-12-30
WINDOW OF SETTING DATE: 1998-12-30
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    FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR PELICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09970076 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       547 PPPNRAPPPSRPPRPSV 564
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ORGANISM: Homo sapiens
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Pred. No. 1e-125;
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PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR PLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-30
PRIOR PLICATION NUMBER: 09/312,359
PRIOR PLICATION NUMBER: 09/312,359
PRIOR PLICATION NUMBER: 09/312,359
PRIOR PLICATION NUMBER: 09/312,369
PRIOR PLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-18
PRIOR PLICATION NUMBER: 09/345,464
PRIOR PLICATION NUMBER: 09/345,464
PRIOR PLICATION NUMBER: 09/345,464
PRIOR PLICATION NUMBER: 09/345,464
PRIOR PLICATION NUMBER: 09/471,179
PRIOR PLICATION NUMBER: 09/471,179
PRIOR PLICATION NUMBER: 09/474,071
PRIOR PLICATION NUMBER: 09/474,071
PRIOR PLICATION NUMBER: 09/474,071
PRIOR PLICATION NUMBER: 09/474,071
PRIOR PLICATION NUMBER: 09/474,072
PRIOR PLICATION NUMBER: 09/474,072
PRIOR PLICATION NUMBER: 09/516,745
PRIOR PRILING DATE: 1999-12-29
PRIOR PRILING DATE: 1999-12-29
PRIOR PRILING DATE: 1999-12-29
PRIOR PRILING DATE: 1999-12-29
PRIOR PLICATION NUMBER: 09/516,745
PRIOR PLICATION NUMBER: 09/516,745
PRIOR PLICATION NUMBER: 09/500,334
PRIOR FILING DATE: 2000-03-01
PRIOR PLICATION NUMBER: 09/500,334
PRIOR FILING DATE: 2000-06-19
PRIOR PLICATION NUMBER: 09/600,565
PRIOR PRILING DATE: 2000-06-19
PRIOR PLING DATE
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Best Local Similarity 98.1%;
Matches 371; Conservative
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Best Local Similarity
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Best Local Similarity 94.8%; Pred. No. 1.9e-117;
Matches 367; Conservative 2; Mismatches 7;
                                                                                                                                   Score 1893.5; DB 1
Pred. No. 1.9e-117;
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Sequence 621, Application US/09833245;
Sequence 621, Application US/09833245
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT FLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER: OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 621
LENGTH 403
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                                                                                                                                         62.6%;
94.8%;
                                                                                                                                                                       Conservative
NUMBER OF SEQ ID NOS: 2267;
SOFWARE: Patentin Ver. 2.;
SEQ ID NO 621
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-11988-621
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Matches 367;
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                                                                                                                          PAPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 201
SOFTWARE: PATENTIN VET. 2.00
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
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                                                                                         Sequence 94, Application PC/TUS0030045 GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.6'
Best Local Similarity 94.8'
Matches 367; Conservative
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PCT-US00-30045-94
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PCT-US01-11988-621
                  361 ESEE 364
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LOCATION: (368) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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llarity 98.6%; Pred. No. 3.7e-116;
Conservative 0; Mismatches 5;
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FOT
CURRENT APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR PELING DATE: 2000-04-12
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEO ID NOS: 2267
SOFTWARE: PATENTIN VET: 2.1
SEO ID NO 620
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OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION:
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OTHER INFORMATION:
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids PCT-US00-30045-125
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                 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM
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Pred. No. 3.7e-116;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: 28 Human Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT:
FURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 98.6%;
Matches 361; Conservative (
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FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa ev
NAME/KEY: SITE
LOCATION: (320)
OTHER INFORMATION: Xaa ev
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa ev
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PCT-US00-30045-125
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-620
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LOCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 3.7e-116;
0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                        Sequence 620, Application US/09833245
; Sequence 620, Application US/09833245
; GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-1
PRIOR FILING DATE: 2000-12-1
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
; SEQ ID NO 620
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Best Local Similarity 98.6%;
Matches 361; Conservative
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August 9, 2002, 10:32:11 ; Search time 119.13 seconds (without alignments) 525.859 Million cell updates/sec
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3025
1 MATAERRALGIGFQWLSLAT......QAPPPNRAPPPSRPPRPSV 564
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Murine TANGO 197.	Human gene 4 encod	Human gene 4 encod	Human TANGO 197.	A human TANGO 216	Amino acid sequenc	A human TANGO 216	A human TANGO 216	A murine TANGO 216	Amino acid sequenc	A murine TANGO 216
	ID	AAB01428	AAE01439	AAE01469	AAB01422	AAB18456	AAB18447	AAB18455	AAB18457	AAB18458	AAB18448	AAB18460
		21	22	22	21	21	21	21	21	21	21	21
	luery Aatch Length DB	381	403	403	333	488	488	488	488	487	487	487
dР	Query Match	66.7	62.6	62.0	54.5	46.7	46.7	46.6	46.6	46.2	46.2	46.1
	Score	2017	1893.5	1874	1649	1412.5	1411.5	1409.5	1408.5	1397.5	1396.5	1395.5
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postnásis, inflammatory bowel diseases, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous Leukemia, cancer, liver disease, Hodgkin's chronic myelogenous Leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic upus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves, Partial Corensic biology, for diagnostic assays, prognostic assays, forensic biology, for diagnostic assays, prognostic assays, corpusptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder;
              Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPARESEEED 366
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Pred: No. 1.9e-151;
3; Mismatches 4;
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                                                                                       Claim 8; Fig 27; 209pp; English
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98.1%;
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Best Local Similarity 98.13
Matches 371; Conservative
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N-PSDB; AAA47479
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XX AAD05300-AAD05379 represent CDNAs corresponding to 28 human secreted protein genes, and AAE0136-AAE01513 represent the proteins they encode. C AAE01514-AAE01544 represent human secreted protein fragments or variants. C AAE01514-AAE01544 represent human secreted protein fragments or variants. C The genes and their secreted proteins are useful for preventing, the genes and their secreted proteins, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the therapy. Pathological conditions can be diagnosed by determining the mutations in the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are most highly expressed, c and include developining products for the diagnosis or treatment of proliferative disorders, diseases of the immune system, about of allegases (e.g., rheumatoid arthritis), inflammation, allegases (e.g., rheumatoid arthritis), inflammation, as the disorders, organizeders, schizophrenia, asthma, extinctions disorders, pregnancy-related disorders, end indisorders, pregnancy-related disorders, end indisorders, pregnancy-related disorders, end indisorders, pregnancy related disorders, and can be used to suburn, to maintain organs before transplantation, for supporting c cognate ligands or binding partners, and in chemotraxis, and can be used c cognate ligands or binding partners, and in chemotraxis, and can be used in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked in diagnostic immunosasays e.g., radioimmunosupers or enzyme tinked in diagnostic immunoscipent assay (ELISA). The present sequence represents a human immunoscipent. New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease, parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; lifection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19. ņ "Mature human secreted protein" Ä Komatsoulis GA, Moore PA, Birse CE, Claim 11; Page 485-486; 562pp; English. 'label= Signal_peptide Location/Qualifiers (HUMA-) HUMAN GENOME SCI INC 05-NOV-1999; 99US-0163581. 30-JUN-2000; 2000US-0215133. 01-NOV-2000; 2000WO-US30045. 28..403 /note= WPI; 2001-308778/32. N-PSDB; AAD05303. WO200134626-A1. Homo sapiens. 17-MAY-2001. Ruben SM, Peptide Protein

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0; Gaps

Sequence

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05-NOV-1999;
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                                                                                                                                              KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
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                                    1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                             Human; secreted protein; proliferative disorder; cancer; tumour;
                    11;
 Length 403;
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                  7; Indels
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 22;
Score 1893.5; DB 2;
Pred. No. 1.3e-141;
2; Mismatches 7;
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/note= "Encoded by
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62.6%;
94.8%;
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Query Match 62.6
Best Local Similarity 94.8
Matches 367; Conservative
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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                         New nucleic acid molecules encoding 2\theta human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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                                                                                                                                                                                                                           Moore PA,
/note= "Encoded by
                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                  01-NOV-2000; 2000WO-US30045.
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                                                                                                                                                                                                                         Komatsoulis GA,
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WPI; 2000-579269/54.
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Best Local Similarity
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                                    333 AA;
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                                                                                                       Matches 318;
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                                      Sequence
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SSX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel diseases, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune classes e.g. myasthemia gravis, autoimmune diabetes and systemic lipse srythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO phyreptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                          TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; chodyfin's disease; myasthemia; Luyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; psystemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; human.
                                                                                                         DGLSFISSSVIITTTHCSDGSILAIALLILFLLIALALLWWFWPLCCTVIIKEVPPPPAE 360
                                                                    300
 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
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                                                                                                                                                                                                                                                               AAB01422 standard; Protein; 333
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                                                                                                                                                                                                                                                                                                                   (first entry)
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N-PSDB; AAA47455.
                                                                                                                                                                                                                                                                                                                                             Human TANGO 197
                                                                                                                                                                      361 ESEEED 366
                                                                                                                                                                                               esevsd 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                     20-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-2000.
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TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                                                                                                                                                                   121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                 1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                                                                                                                                                                                          disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
                                                                                                                                                                                         ö
                                                                                                                                        Length 333;
                                                                                                                                                                                         Indels
                                                                                                                                          54.5%; Score 1649; DB 21;
100.0%; Pred. No. 2.2e-122;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser CC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB18456 standard; Protein; 488 AA.
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                                                                                                                                                                                                   Conservative
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AAB18447 standard; Protein; 488

RESULT AAB18447

(first entry)

15-JAN-2001

AAB18447;

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describes TANGO 266, TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 261, TANGO 262, and TANGO 267. The TANGO cellular differentiation modulate cellular spoiliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial estima and bronchiectasis, intestinal disorders, spleen associated diseases, modulate the proliferation, differentiation, as isobment heart disease, modulate the proliferation discretts bone and/or cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to hydrocephalus, brain herniations, iatrogenic disease, inflammations, hydrocephalus, brain herniations, iatrogenic disease, inflammations, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                 -; 175pp; English.
                                                   for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488 AA;
                                                                                               Disclosure; Page
                                                      e.g.
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Gaps Length 488; 46.7%; Score 1412.5; DB 21; Length 55.6%; Pred. No. 2e-103; ive 77; Mismatches 123; Indels Conservative Similarity Query Match Best Local Simi Matches 274;

Sequence

4; 63 YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG 302 LSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAEES 362 QEYEFPEPRNLNNNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVMRPQ 474 4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI 62 PGDTGRCINFTRV 487 123 183 361 63 181 243 241 303 363 123 121 q g q 셤 g õ g ò ò ð g ò ð g à à

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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; purmonary conqestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; hydrocephalus; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO Polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular dahesion. The proteins can be used to treat any von Willebrand factor associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                              FANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                                                                                                                                                                                                                              "von Willebrand factor A domain"
                                                              Amino acid sequence of human TANGO 216 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..341
Le= "transnmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                 "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                    /note= "signal peptide"
34..79
                                                                                                                                                                                                                                                                                                                                                                                              "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "cytoplasmic
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Fig 1A-C; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
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342..48
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N-PSDB; AAA75149.
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                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                   Domain
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treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or ocedema, emphysema, chronic bronchilaris, bronchilar asthma and bronchictasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders undo and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or they may also be used to treat disorders associated with the disorder. They may also be used to treat disorders associated with the disease, inflammations, bacterial and viral meniations, latrogenic disease, inflammations, bacterial and viral meniatis, Alzheimer's batancase, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, associated and complaintis, and treat hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 keeeeeplptkkwptvdasyyggrgvggikrmevrwgdkgsteegarlekaknavvkipe 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 grgfmlgsrngsvlctytvnetyttsvkpvsvqlnsmlcpapilnkagetldvsvsfngg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSFISSSVIITTHGSDGSILAIALLIFLLLALALLWWFWPLCCTVIIKEVPPPPAEES 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 EEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                    4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI
                                                                                                                                                                                                                                                                                                                  DB 21; Length 488;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.6%; Pred. No. 2.3e-103; Matches 274; Conservative 77; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB18455 standard; Protein; 488 AA.
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                                                                                                                                                                                                                                                                            488 AA;
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                                                                                                                                                                                                                                                                             Sequence
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AAB18455
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 261, TANGO 262, and TANGO 267. The TANGO 267 closures and be used to modulate cellular adhesion. The polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The disorder, regulate extracellular matrix structuring, cellular adhesion, disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, and cellular interactions, and cellular appear in the bone marrow, and leukocytes, treat bone marrow, blood that appear in the bone marrow, and leukocytes, treat bone marrow, blood cellular interaction or codema, emphysema, chronic bronchitis, bronchiticated diseases and disorders, spleen associated casthma and bronchiectasis, intestinal disorders, spleen associated casthma and bronchiectasis, intestinal disorders, spleen associated conduct function of bone and cartilage cells and to treat bone and cartilage cells and to treat bone and cartilage cells and to treat bone and cartilage cells and to treat disorders associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. Disease, cerebral bacterial and viral meningitis, all the worles are cerebral careted using information provided.
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 ISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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; Mismatches 115; Indels
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56.2%; Pre-
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Matches 271; Conserv
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
on Willebrand factor associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                             485
                                                                                                                  314 TTHCSDGSILAIALLILELLLALALLWWFWPLCCTVIIKEVPPPPAEESEEEDDDGLPKK 373
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SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells modulate the proliferation, differentiation on of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysemm, chronic bronchills, bronchlal sthma and bronchiectasis, intestinal disorders, spleen associated disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder, They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, all allocated disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
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55.4%; Pred. No. 4.1e-103;
1ive 78; Mismatches 123; Indels
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Best Local Similarity 55.4%
Matches 273; Conservative
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Created using information provided.
                                                                            rango 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; schemic heart disease; rhydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; higheriner's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                              A murine TANGO 216 polypeptide clone.
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cellular proliferation; cellular differentiation; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; hematopoietic associated disease; atelectrasis; pulmonary congestion; intestinal disorder; spheen associated disease; renal disorder; spheen associated disease; renal disorder; schemic heart disease; hydrocephalus; brain hernation; atrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                       TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
Amino acid sequence of a murine TANGO 216 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "transnmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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342..48
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/note=
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Gaps

21;

DB 21; Length 487;

46.2%; Score 1397.5; DB 21; Length 54.8%; Pred. No. 3e-102; Live 72; Mismatches 131; Indels

Conservative

272;

Similarity

Query Match

Local

Best Loc Matches

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1 MATAERRALGIGFQWLSLATLVLICAGOGG-RREDGGPACYGGFDLYFILDKSGSVLHHW

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                     Fraser CC;
                                                                                                                                                                                                     Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Fig 2A-C; 175pp; English.
                                                                                                                                           (MILL-) MILLENNIUM PHARM INC.
                           01-MAR-2000; 2000WO-US05226.
                                                                                  99US-0122458.
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                                                                                                                                                                                                                                                         WPI; 2000-579269/54.
N-PSDB; AAA75150.
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                                                                                  01-MAR-1999;
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Matches 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO cestibles TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cecllular describe used to modulate cellular adhesion. modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, cand hematopoietic associated diseases and disorders, spleen associated asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                  420 MPEQEYEFPEPRNLNNNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVM 471
ndgksavsrsltitatectngiaaivailvlllllgaalmwwfwplcckvvikdppppps 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                          360 EESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser CC;
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                                                                                                                                                                                                                                                                                                                                                                AAB18460 standard; Protein; 487 AA.
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                                                                                                                                                                                                                472 RPQPGDTGRCINFTRV 487
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rpqegdegrcinfsrv 484
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  298
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as ischemic heart disease, modulate the proliferation, differentiation and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral cedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. In once: the present sequence does not appear in the specification; it was created using information provided.
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                                                                                                                                                                                                                                                                                                                                       Length 487;
                                                                                                                                                                                                                                                 46.1%; Score 1395.5; DB 21; Lengt
54.8%; Pred. No. 4.3e-102;
ive 72; Mismatches 131; Indels
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                                                                                                                                                                                                                                                                             Similarity
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Matches 272;
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 closed and be used to modulate cellular adhesion. The polypeptides can be used to treat any von Willabrand factor-associated reclular differentiation and/or modulate cellular adhesion. The cellular adhesion. The and cell trafficking and/or migration, modulate cellular interactions, and cell trafficking and/or infartative disorders, such as cancer, condulate the proliferation of differentiation, and/or function of cells modulate the proliferation, differentiation, and/or function of cells culmonary congestion or ocdems, emphysems, chronic bronchitis, bronchitectasis, intestinal disorders, spleen associated associated disease, modulate renal disorders, treat cardiovascular disorders such disorders associated disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, differentiation, differentiation, differentiation, differentiations, treat disorders associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases, multiple schemic disease, inflammations, toxoplasmosis, parkinson's disease, multiple schemic erebal cartilage change the present sequence does not appear in the specification; it was occaping the present sequence does not appear in the specification; it was created using information provided.
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54.6%; Pred. No. 6.2e-102;
.ive 73; Mismatches 131; Indels
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                                                                                                                                                                                                                                                                                           Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                             Sharp
                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                   99US-0122458.
                                                                                                                                                                               01-MAR-2000; 2000WO-US05226.
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31-JAN-2000; 2000US-0179065.04-FEB-2000; 2000US-0180628.
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                                                                                                                                                                                                                specification.
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                                                                                                                                                                                                                                                    peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Heamostetic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides, useful for treating disorders
                                                                                                       VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM
                                   NDGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPA
                                                                                                                                                          360 EESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVK
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Zhang J;
                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy;
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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14-SEP-2000;
19-OCT-2000;
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25-APR-2000;
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system coalised neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibhin activity, chemotactic/chemotantic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                ombolytic activity, cancer diagnosis and therapy, drug screening, for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                 \textsc{c.N.S} disorders. Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 297;
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Pred. No. 4.3e-102;
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Matches 267; Conservative
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US-0184664 US-0186550 US-0186750 US-018974 US-02196075 US-0210467 US-02164647 US-02164647 US-021648647 US-021648647 US-021648647 US-021648647 US-021648647 US-021648647 US-021647 US-021648647 US-021648647 US-021648647 US-02164647 US-021748687 US-02174887 US-02174887 US-02174887 US-02174887 US-02174887 US-02174887	2000US-0224519. 2000US-022514. 2000US-022514. 2000US-022526. 2000US-022526. 2000US-022526. 2000US-0225270. 2000US-0225770. 2000US-0225778. 2000US-022578. 2000US-022578. 2000US-022578. 2000US-022578. 2000US-022578. 2000US-022578. 2000US-022934.	000S-02313 000S-02313 000S-02313 000S-02313 000S-02324 000S-02324 000S-02330 000S-02330 000S-0234 000S-0234 000S-0234 000S-0234 000S-0234 000S-0234 000S-0234
EB-2000; 20 IAR-2000; 20	14-AUG-2000; 2000 14-AUG-2000; 2000 14-AUG-2000; 200 14-AUG-2000; 200 14-AUG-2000; 200 14-AUG-2000; 200 14-AUG-2000; 200 14-AUG-2000; 200 14-AUG-2000; 200 18-AUG-2000; 200 18-AUG-2000; 200 22-AUG-2000; 200 22-AUG-2000; 200 22-AUG-2000; 200 23-AUG-2000; 200 23-AUG-2000; 200 01-SEP-2000; 200 01-SEP-2000; 200 01-SEP-2000; 200 01-SEP-2000; 200 06-SEP-2000; 200	SEP-2000; -SEP-2000; -
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                                     The invention retaced extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, dass, dogs, chickens or sheep. For example, disorders associated with decreased extracellular shears associated with decreased expression of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to treat diseases by gene therapy. The SPS may also be used as DNA probes in diagnostic assays. The SPS may also be used as antigens to produce antibodies and to identify modulators used as antigens to produce antibodies and to identify modulators (agonists and antigonists) of the SPS. The anti (SP) antibodies and antagonists may also be used to down regulate expression and activity of SPS and as disquostic agents for detecting the presence of SPS in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperporoliferative disorders (e.g. cancher's disease) neurological diseases (e.g. Alzheimer's disease, cancher's disease) ardio-'Cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 TTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEESEEEDDDGLPKK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 wlfpglwllvlsgpggllraqeqpscrrafdlyfvldksgsvanxwieiynfvqqlaerf 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQCLEELQKVLPGGDTYMHEGFERASEQIYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to isolated nucleic acid molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                  Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.9%; Score 1206.5; DB 22; Lengtl
Best Local Similarity 56.2%; Pred. No. 5.1e-87;
Matches 232; Conservative 67; Mismatches 111; Indels
SEQ ID No 312; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein sequence SEQ ID NO:11706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB92985 standard; Protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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   Claim 11;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary trand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 1-end sequence, where the opinionucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynocleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13618 and AAH13633 to AAH13624 and AAH13633 to AAH13632 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 139
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                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                             aito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 11706; 2537pp + CD ROM; English.
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Pred. No. 1.5e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                           Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                               99JP-0300253.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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98.9%;
                                                                                                             2000EP-0116126
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Best Local Similarity 98.9
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs -
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|kindsvt.lsk 190
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09-JUN-2000;
EP1074617-A2
                                                                                                             28-JUL-2000;
                                                                                                                                                                                                                           11-JAN-2000;
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                                                        07-FEB-2001
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Search completed: August 9, 2002, 10:32:13 Job time: 132 sec

us-09-970-076-6.rag

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us-09-970-076-6.rpr

- protein search, using sw model OM protein

Search time 61.73 Seconds ٠. August 9, 2002, 10:34:15 Run on:

(without alignments) 877.926 Million cell updates/sec

Title:

US-09-970-076-6 3025 1 MATAERRALGIGFQWLSLAT......QAPPPNRAPPPSRPPRPSV Perfect score: Sequence:

564

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR_71:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	extensin homolog T	hypothetical prote	pherophorin-S - Vo	extensin - Volvox	unknown protein [i	hypothetical prote	collagen alpha 1(x		sulfated surface g	extensin-like prot	hypothetical proli	extensin homolog F	hypothetical prote	extensin class I (extensin precursor	extensin class 1 p	hypothetical prote	extensin precursor	extensin (clone To	hydroxyproline-ric	formin isoform IV	formin - mouse	hydroxyproline-ric	extensin-like cell	proline-rich cell	extensin-like prot	chitinase (EC 3.2.	hydroxyproline-ric
ID	F96531	T06291	B96534	T10798	S22697	G86441	AE2295	A40020	T51947	A33647	S54156	A34043	T05225	C84534	S14974	A24354	T11622	D96711	825299	S25298	C29356	S24407	S11515	A29356	T10737	T09854	T11671	S51939	806733
BB :	7	7	N	7	a	N	~	-	~	7	7	7	7	7	~	N	~	~	7	~	7	7	7	~	7	~	~	~	~
Ouery Match Length	847	760	464	599	464	1201	383	3124	1392	485	242	141	669	727	181	306	489	708	322	388	368	1206	1468	163	214	214	280	439	620
Ouery Match	7.5	9.8	8.9	6.7	6.7	9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.5	6.4	6.3	6.3	6.3	6.3	6.3	6.3	6.2	6.2		6.2	6.1	6.1	6.1	6.1	6.1
Score	227	205.5	202	203	202	201	200.5	200.5	199.5	199	198	197.5	195.5	194	191.5	191.5	191.5	191.5	191	189.5	189	188.5	•	186.5	186	8	186	ď.	185.5
Result No.	н	7	9	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

probable extensin	Wiskott-Aldrich sy	extensin-like prot	extensin class I (extensin homolog H	extensin - almond	probable Pto kinas	extensin homolog F	extensin class I (extensin CYC15 pre	extensin precursor	hypothetical prote	extensin class I (hydroxyproline-ric	hypothetical prote	hypothetical prote
F84862	A55197	S49915	S14970	T07623	820790	F86387	T01456	S14981	T09964	T10863	E96636	S14972	A25494	D84672	T16342
7	7	7	~	~	~	N	7	~	7	~	~	~	~	7	7
212	205	1188	132	169	278	160	186	199	225	580	907	90	93	134	250
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0.9	0.9	9.0	9	9.0	9.0	6.0	9.0	9	6.0	6.0	9.0	6.0	5.9	5.9	5.9
_	182.5 6.0														

ALIGNMENTS

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Pybb31
hypothetical protein F13F21.7 (imported) - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: F95531
C; Filly M; Hughas, B; Hughes, Hug

13; Gaps 355 PPPPAEES----EEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKL 410 411 EKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKW------YSPIKGKLDALWV 459 460 LLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAP 519 520 HCPPPPP-SAPTPP---IPSPPSTLPPPPQAPPNRAPPP-----SRPPPRP 562 475 EQPKPEESPKPEQP-QIPEP----TKPVSPPNEAQGPTPDDPYDASPVK-----88; Length 847; Indels 60; Ouery Match 7.5%; Score 227; DB 2; Best Local Similarity 31.5%; Pred. No. 3.7e-07; Matches 75; Conservative 15; Mismatches 60 557 QΩ qq 염 δ δ Q ò ò

RESULT T06291

extensin homolog T9E8.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)

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Gaps

4;

Length 599; Indels

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C;Species: Volvox carteri
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jul-2000
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jul-2000
C;Accession: 222697; 821006
R;Ert, H.; Hallmann, A.; Wenzl, S.; Sumper, M.
BMBO J: 11, 2055-2062, 1992
A;Title: A novel extensin that may organize extracellular matrix biogenesis in Volvox
A;Reference number: $22697; MuID:92289669
A;Accession: $22697...
C;Accession: T10798
R;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophori A;Reference number: Z17154; MUID:97162277
A;Accession: T10798
A;Actatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-599 <GGDD>A;Residues: 1-599 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Residues: 1-590 <GGD>A;Re
                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:V07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Cross-references: Extrain HK 10; sub_species Nagariensis
A;Experimental socurce: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-c;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RVKM----PEQEYEFPEPRNLNNMRRPS 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 LQGIIHSILKK----SCIEILAAEPST--ICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 INDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFI---SSSVIITTHC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 PLNNAYHTSSPPPAPIYTPPPPAPHCPPPPSAPTPPIPSPPSTLPPPPQAPPNRAPPP 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Mesidues: 1-464 <HAL>
A; Cross-references: EMBL:X65165; NID:g21991; PIDN:CAA46283.1; PID:g21992
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 ADIVADSKNTVALVTAAAVVVQTTPSPPPPRVSTSPPPPARVSSSPPPATRSPPPRRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 SDGSILAIALLILFLLLALALWWFWPLCC-----TVIIKEVPPP-----PAEESEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PKKKWPTVDASYYGGRGVGGIKRMEVRW--GEKGSTEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 202; DB 2; Length 464
; Pred. No. 7.6e-06;
46; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 203; DB 2; L
Pred. No. 9.1e-06;
1; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extensin - Volvox carteri (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o. 178;
Similarity 23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.7%;
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556 SRPPPRPS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 PPPPPPS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simi
Matches 100;
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                               C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999
C; Accession: T0629;
C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999
C; Accession: T0620;
A; Reference number: 21558
A; Accession: T0629;
A; Molecule type: DNA
A; Residues: 1-760 CBEV-
A; Cross-references: EMBL:AL049608
A; Experimental source: cultivar Columbia; BAC clone T9E8
C; Genetics:
C; Genetics:
A; Map position: 4
A; Note: T9E8.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pherophorin-S - Volvox carteri
C;Species: Volvox carteri
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498 NNAYHTSSPPPAP---IYTPPPPAPHCPPPPSAPTPPIPSPFSTLPPPPQAPPNRAPP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503 TSSPPPA---PIYTPPPPAP-----HCPPPPPSAPTPPIPSPPSTLPPPPQAPPPNRAP
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Pred. No. 5.2e-06;
5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 205.5; DB 2
Pred. No. 8.5e-06;
4; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.8%;
Best Local Similarity 53.5%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 55.19
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 PPSPPPPPPV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: | |:||
PAPPKPQPS 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-494 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B96534
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Best Local S:
Matches 38;
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T10798
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22;

Length 464;

407

364

4

Gaps

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Collagen alpha I(XII) chain precursor - chicken

Natternate names: fibrochimerin

C; Species: Gallus gallus (chicken)

C; Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811

R; Yamagata, M.; Yamada, K.M.; Dublet, B.; Van der Rest, M.; Olsen, B.R.

R; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; Van der Rest, M.; Olsen, B.R.

A; Reference number: A34485; MUID: 90062079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
B;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of peps A;Reference number: $22254; MUID:88087065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 2960-2976, F', 2978-3074,'AG' <GOR3>
A; Residues: 2960-2976, F', 2978-3074,'AG' <GOR3>
A; Cross-references: EMBL:M1375; NID:9211649; PIDN:AAA48718.1; PID:9211650
A; Note: this sequence has been revised in reference A34485
B; Koch, M; Bernasconi, C; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel large form
A; Reference number: S23814; MUID:92362621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 2772-2793; 2846-2873 <GOR2>
A; Residues: 2772-2793; 2846-2873 <GOR2>
B; Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A; Title: Type XII collagen: distinct extracellular matrix component discovered A; Reference number: A28037; MUID:87317590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A;Residues: 2456-2788,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
                                                                                                                                                                                                                                     449 PIKGKLDALWVLLRKGYDRVSVMRPQPGDTG--RCINFTRVKNNQPAKYPLNNAYHTSSP 506
                                                                                                                                                                                                                                                                           274 PINSLVDIGEFLEQNG------QQLGNDGDINDIN-NNINNVQPDPPPPSDPPPDP
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                                                                                                                                 Length 383;
                                                                                                                                                                                       Indels
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A; Molecule type: protein
A; Residues: 2831-2832, T', 2834, R', 2836-2843; 3002-3014
                                                                                                                                      DB 2;
                                                                                                                                    Score 200.5; DB 2 Pred. No. 7.4e-06;
                                                                                                                                                                                       6; Mismatches
A; Experimental source: strain PCC 7120 C; Genetics:
A; Gene: all3916
                                                                                                                                    6.6%;
                                                                                                                                 Query Match 6.6
Best Local Similarity 40.5
Matches 47; Conservative
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A; Note: Anabaena sp.
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C; Accession: AE2295
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                12;
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A;Molecule type: DNA
A;Residues: 1-383 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75615.1; PID:g17133050; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-1201 <STO>
A; Cross-references: GB: AEO05172; NID: 911136725; PIDN: AAG31306.1; GSPDB: GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            407 SSDEG--FEAIQRPRIHIPFDNDDTDDITLSVAHESSEEPHEFSHHHHHEIPAKDSVDNP 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 CP----PPPPSAPTPPIPS----PPSTLPPPPQAPPNRAPP-----PSRPPPRP 562
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Pred. No. 3.1e-05;
1; Mismatches 53;
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26.2%; Pred
tive 24;
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                                                                                                                                                         358 SPPPVVSPPPPP 371
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Best Local Similarity
Matches 62; Conserv
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probable transcription factor HUA2 [imported] - Arabidopsis thaliana probable transcription factor HUA2 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) c; pate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C; Accession: T51947 E.Chen, X; Meyerowitz, E.M.

Richen, X; Meyerowitz, E.M.

Mol. Cell 3, 349-360, 1999
A; Title: HUA1 and HUA2 are two members of the floral homeotic AGAMOUS pathway. A; Reference number: 225882; MUID:99214850
A; Title: HUA1 and HUA2 are two members of the floral homeotic AGAMOUS pathway. A; Reference number: 125882; MUID:99214850
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKM 420
                                                                                                                                                                                                                                                                                                                        2643 EVKKIFYGSFHKVHIVVTSSNVKIYIDCSEILEKPIKEAGNITTDGYEILGKLLKGDRRS 2702
                                                                                                                                                                                                                                                          PSSPRKWY-----SPIK--GKL--DALWVL--LRKGYDRV 468
                                                                                                                               376 PIVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYEFPEPRNLNN 435
HCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAEESEEEDDDGLPKKKW 375
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                                                                                                                                                                                             2602 QITDRDYKPQVGV-----VLDPGSKVLSFFNKDTRGEVQTVTFD----ND
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31.3%; Pred. No. 4.7e-05;
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A;Map position:
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A; Status; preliminary
A; Molecule type: MRNA
A; Residues: 1-44,1189-11257, 87,1259-1263, F2,1265-1280 <TRU>
A; Cross-references: EMBL: 8673; 2889/3; 2899/3; 2895/1; 3008/1; 3065/1
C; Genetics:
C; Genetics:
A; Introns 2845/3; 2863/3; 2889/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
A; Introns 2845/3; 2863/3; 2889/3; 2895/1; 3008/1; 3065/1
C; Superfamily: collagen alpha I(XII) chain if intronectin type III repeat homology colled coil: connective tissue; disulfice F1-23/Domain: signal sequence has 1(XII) chain is status predicted colled coil: connective tissue; disulfice F1-23/Domain: if ibronectin type III repeat homology <FN3A>
F2-114/Domain: if ibronectin type III repeat homology colled colled first first first status predicted <IIIIC>
F2-117-30/Domain: iIII status predicted <IIIIC>
F2-117-30/Domain: iIII status predicted <IIIIC>
F2-118-30/Domain: iIII status predicted <IIIIC>
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F;2903-2945/Domain: cell attachment (R-G-D) motif
F;2946-3048/Domain: collagenous COLI #status predicted <COLI>
F;3046-3124/Domain: non-collagenous NC1 #status predicted <NCI>
F;3046-3124/Domain: non-collagenous NC1 #status predicted <NCI>
F;3046-3124/Domain: non-collagenous NC1 #status predicted <NCI>
F;3049-3124/Domain: hydroxyproline F;2780,2789,2836,2860,2866,2869,3004,3007/Modified site: hydroxyproline
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21.8%; Pred. No. 0.00012;
Live 76; Mismatches 204; Indels 237;
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Best Local Similarity 21.8
Matches 144; Conservative
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A; Reference number: A90159; MUID: 90147742
                                     A Accession: A34043
A Molecule type: DNA
A, Residues: 1-141 cBAK>
A, Cross references: GB:M32217
A, Accession: B34043
A, Molecule type: DNA
A, Residues: 59-136 cBAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4
A; Note: F17I5.160
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A;Map position: 2
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C;Species: Vigna unguiculata (cowpea)
C;Species: Vigna unguiculata (cowpea)
C;Species: Vigna unguiculata (cowpea)
C;Date: (08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 11-Jan-2000
C;Accession: 554156
R;Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.
Submitted to the EMBL Data Library, April 1995
A;Description: A class of root-hair specific extensins involved in rhizobium/legume inte
A;Reference number: 554155
A;Accession: 554156
                                                                                                                                                      RETL, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
J. Cell Biol. 109, 3493-3501, 1989
J. Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A; Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A; Reference number: A33647; MUID:90094551
J. Reference number: A33647
J. Status: preliminary
J. Status: preliminary
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J. Status: preliminary
J. Status: preliminary
J. Status: RNA
J. Residues: 1-485 < CERT>
J. Status: CERT>
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C; Species: Owenia fusiformis
C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
C; Accession: A34043; B34043
R; Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A;Title: Presence in invertebrate genomes of sequences characterized by the repetition
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                             C;Species: Volvox carteri
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A33647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 DIGRCINFTRVKNNQPAKYPLNNAYHISSPPPAP-----IYTPPPPAPHCPP----- 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPSA 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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A;Molecule type: mRNA
A;Residues: 1-242 AARS>
A;Cross-references: EMBL:X86029; NID:9791147; PID:9791148
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 199; DB 2;
Pred. No. 1.3e-05;
    surface glycoprotein 185 - Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTPPIPSPPSTLPPPPQAPPNRAPPPSRPPRPS 563
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Best Local Similarity 44.2%;
Matches 42; Conservative
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: 105225
C;Accession: 105225
Submitted to the Protein Sequence Database, July 1998
A;Reference number: 215404
A;Recerence number: 215404
A;Recerence number: 215404
A;Recience Total Sequence Database, July 1998
A;Recience number: 215404
A;Recession: 105225
A;Molecule type: DNA
A;Residues: 1-699 <BEV>
A;Residues: 1-699 <BEV>
A;Residues: 1-699 <BEV>
A;Residues: 1-699 <BEV>
A;Residues: 1-699 <BEV>
A;Resperimental source: cultivar Columbia; BAC clone F1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g15880 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Spate: 102-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spate: 102-102) (Spa
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C;Genetics:
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                                                                                                                           18;
                DB 2;
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Score 197.5; DB 2
Pred. No. 3.2e-06;
2; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.5%; Score 195.5; DB 2
Best Local Similarity 42.7%; Pred. No. 3.5e-05;
Matches 47; Conservative 9; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extensin homolog F1715.160 - Arabidopsis thaliana
                6.5%;
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extensin class I (clone uG-18) - tomato (fragment)
extensin class I (clone uG-18) - tomato (fragment)
c; Species: Lycopersicon esculentum (tomato)
c; Species: Urcopersicon esculentum (tomato)
c; Species: D7-May-1998 #sequence_revision 15-May-1998 #text_change 21-Jul-2000
c; Accession: S14974
c; Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A; Title: Tomato extensin and extensin-like cDNAs: structure and expression in response the A; Reference number: S14970; MUID:91329690
A; Reference number: S14974
A; Reference number: S14970; MUID:91329690
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-181 < SHO
A; Cross-references: EMBL:X55685; NID:g19229; PIDN:CAA39215.1; PID:g1345537
A; Cross-references: EMBL:X55685; NID:g19229; PIDN:CAA39215.1; PID:g1345537
C; Superfamily: hydroxyproline-rich glycoprotein; hydroxyproline
C; Reywords: cell wall; glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 PEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGR 480
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                                                                                                                                                                                     473 PQPGD---TGRCINFT--RVKNNQPAK---YPLNNAYHTS-----SPPPAPIYTPPPPA 518
                                                                                                                                                                                                                 406 VHKPQPPKESPQPNDPYNQSPVKFRRSPPPPQQPHHHV-----------VHS 446
                                                                                           418 VKMPEQEYEFPEPRNLNNN-----MRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMR 472
                                                     Gaps
                                                                                                                                                                                                                                                                              519 P-HCPPPPP---SAPTPPIPSPP----STLPPPP--QAPPPNRAPPP---SRPPP 560
                                                                                                                                                                                                                                                                                                        48; Indels 54;
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ch 6.4%; Score 194; DB 2; Length 727; 1 Similarity 33.3%; Pred. No. 4.6e-05; 59; Conservative 16; Mismatches 48; Indels 5
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Best Local Similarity 29.8%; Pred. No. 1.1e-05;
Matches 51; Conservative 12; Mismatches 35.
                     Query Match
Best Local Similarity
Matches 59; Conserva
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Search completed: August 9, 2002, 10:34:18 Job time: 257 sec

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Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.;
"Identification of the Cellular Receptor for Anthrax Toxin.";
Nature 414:0-0(2001).
EMBL; AF421380; AAL26496.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 2.4e-150;
ive 0; Mismatches 0; Indels
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Last annotation update)
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Eukaryota; Metazoa; Chordata;
Query Match
Best Local Similarity 100.0
Matches 364; Conservative
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0948y6 volvox cart
095bml volvox cart
09f1q7 arabidopsis
09f1q7 arabidopsis
09fxal arabidopsis
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Q96nc7 homo sapien
Q96ec6 homo sapien
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                    9, 2002, 10:46:21
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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230 CTFG 233
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPR---- 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 EKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDGSILAIALL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ31074 FIS, CLONE HSYRA2001476.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
    SEQUENCE FROM N.A.
TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
TISSUE.;
                                                                                                                                                                                                                                                                                                                                                                                                 24.7%; Score 746.5; DB 11; Length 221; 59.9%; Pred. No. 1.6e-54; Live 30; Mismatches 44; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003908; AAH03908.1; ...
                                                                                                                                                                                                                                                                                                                                                                       221 AA; 24505 MW; 31AB702E42E9CEB3 CRC64;
                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 24.5 KDA PROTEIN (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                    221 AA
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 59.99
Matches 136; Conservative
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                                                                                                                                                                                      PRELIMINARY;
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361 ESEE 364
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Q99L17;
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FQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQ 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 GYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDH 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 VFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 TYTVNETYTTSVKPVSVQLNSMLCPAPILNKAG------EWGLTVTQAGVKWHDLTH 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 LRMSFIVFSTRGTILMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRO 137
Ninomiya K., Wagatsuma M., Kahda K., Kondo H., Yokoi T., Kodaira H., Ninomiya K., Wagatsuma M., Yahamazaki M., Sugiyama T., Tiek R., Katsuta N., Sato K., Tanikawa M., Yahamazaki M., Sugiyama T., Irie R., Ostsuta N., Sato H., Hakamatsu A., Ishii S., Yamamoto J., Isono Y., Csuki T., Sato H., Washatsu A., Ishii S., Yamanoto J., Isono Y., Kawai Hio Y., Satto K., Nishikawa T., Kiluchi H., Murakawa K., Yamashita H., Murakuo K., Nakamura Y., Sekine M., Kiluchi H., Murakawa K., Yamashita H., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Supinited (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO55636; BAB70976.1; BIREGEBOAZEBEEGG CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                             Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                      67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC012475; AAH12475.1; -.
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Pred. No. 2.6e-25;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                     19.0%; Score 574; DB 4;
49.2%; Pred. No. 5.1e-40;
vative 45; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.0%
Best Local Similarity 49.2%
Matches 120; Conservative
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Best Local Similarity
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9

Gaps

39;

Length 687;

618

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RESULT 09XIB6

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thaliana chromosome 3. II. 4,251,695 bp covered by ninety Pl,
                                                                                                                                                                                                                                                                                                                                                                                                                428 PEPRNLNNNMRRPSSPR-------KWYSPIKGKLDALWVLLRKGYDRVSVMR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 19, Last annotation update)
EXTENSIN PROTEIN-LIKE.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplanatae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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          SEVENCE.

STRAIN-HK 10;

MEDLINE-21382906; PubMed-11489172;

Hallmann A., Amon P., Godl K., Heltzer M., Sumper M.;

Hallmann A., Amon P., Godl K., Heltzer M., Sumper M.;

Hallmann A., Amon P., Godl R., Heltzer M., Sumper M.;

Hydroxy)protline-rich and metalloproteinase homology domains.";

EMBL; AJ311549; CAC39318.1;

SEQUENCE 687 AA: 72017 MW; 6DD95714C350B3CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 PSPRPPRRPPRPSSPRPPPDDPSPPPSPPTSP--SPPDPAWANLPTSPDPPSPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 PQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPSAPTPP
                                                                                                                                                                                                                                                                                                            Score 213.5; DB 10; Length
Pred. No. 3.6e-09;
5; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., T. Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
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; E34E185E63BB47C3 CRC64;
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27.1%; Pred. No. 6.3e-09;
iive 27; Mismatches 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura Y.;
"Structural analysis of Arabidopsis tha."
Sequence features of the regions of 4,22
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP000735; BAB01698.1; -.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR0013692; LRR_out.
InterPro; IPR0013692; Pritch_extensin.
InterPro; IPR002965; Pritch_extensin.
PRINTS; PR01217; PRICHEXTENSIN.
PRINTS; SM01218; PSTLEXTENSIN.
SMART; SM00370; LRR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 PPSPPPPSPPPSPPPN-PPPPSPPSP 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 IPSPPSTLPPPPQAPPNRAPPPSRPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=COLUMBIA;
MEDLINE-20363099; PubMed-10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102822 MW;
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                                                                                                                                                                                                                                                                                                               7.18;
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                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 37.3
Matches 56; Conservative
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SEQUENCE
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Q9LJ64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPPPAEES----EEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 PQPPKHESPKPEEPENKHELPKQK--------ESPKPQPSKPEDSPKP 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 EKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKW------YSPIKGKLDALWV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 LLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAP 519
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Sukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3068;
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Pred. No. 3.5e-10;
                                                                                                                                 847 AA
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61 VSMNDGLSFISSSVIITTT---QGSLHKIA
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01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001)
                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, F13F21.7 PROTEIN.
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Query Match

Best Loc Matches 355

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Best Local Similarity
Matches 74; Conserva
                                                                                                                                                                                                                                                                                                                           409 AA;
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nes 40; Conser
SEQUENCE FROM N.A. STRAIN=HK10;
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        EEGAKLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKG 464
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Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxiD=3068;
                                                                                                                                                                                       614 YDASPIKKRRPOPPSP----STEETKTTSPQSPPVHSPPPPPVHSPPPPWFSPPPMHS
                                                                                                                                                                                                                               SSP----PPAPIXTPPPPAPHCPPPPSAPTPPIPSPPSTL-----PPPP--QAPP
                                                                                                                                                                                                                                                       Volvox carteri f. nagariensis.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3068;
                                                                                               EESPKPQPPKQETPK-PE---ESPKPQ-----PPKQEQPPKTEAPKMGSPPLESPVPNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-HK 10;
MEDLINE-21382906; PubMed-11489172;
Hallmann A., Amon P., Godl K., Heitzer M., Sumper M.;
Hallmann A., Amon P., Godl K., Heitzer M., Sumper M.;
Hallmann A., Amon P., Godl K., Heitzer M., Sumper M.;
Hydroxiptional activation by the sexual pheromone and wounding new gene family from Volvox encoding modular proteins with (hydroxy)proline-rich and metalloproteinase homology domains.";
(hydroxy)proline-rich and metalloproteinase homology domains.";
Plant J. 26:583-593(2001).
EMBL; AJ311550; CAC39319.1;
SEQUENCE 1143 AA; 123155 MW; OCEOFD2CED52200C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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ilarity 51.9%; Pred. No. 8.1e-09;
Conservative 5; Mismatches 30;
                                                                                                                                                     YDR--VSVMRPQPGDTGRCINFTRVKNNQPAKYPLNN----
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01-DEC-2001 (TTEMBLEEL: 19,
01-DEC-2001 (TTEMBLEEL: 19,
01-DEC-2001 (TTEMBLEEL: 19,
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Best Local Similarity
Matches 40; Conserv
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SEQUENCE FROM N.A.
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Q9SBM1
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Q948Y6
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GB|AAD23008 1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                       HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP.
CD0749C6AF02BD74 CRC64;
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DNA Res. 5:4.154(1998).

ENBL: AB010070; BAB11454.1;

InterPro: IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-2004/763; PubMed-10574980;
MEDLINE-20044763; PubMed-10574980;
MEDLINE-20044763; Amon P., Sumper M.;
"Response to the sexual pheromone and wounding in the green alga "Response to the sexual pheromone and wounding in the green alga Volyox; induction of an extracellular glycoprotein consisting almost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 120;
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b; IPR002965; P_itch_extensn.
PR01217; PRICHEXTENSN.
1289 AA; 137558 MW; 898E55A2A618F5E0 CRC64;
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23.9%; Pred. No. 1.4e-08;
tive 24; Mismatches 91;
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Pred. No. 2.7e-09;
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                                                                                                              exclusively of hydroxyproline.";
J. Biol. Chem. 274:35023-35028(1999).
EMBL; AJ242540; CAB6228011;
Interpro; IPR003882; Pistil_extensin.
InterPro; IPR002965; P.ich_extensin.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-COLUMBIA;
MEDLINE-98290546; PubMed-9628582;
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409 HX
41547 MW;
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867 498 927

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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 NNAYHTSSPPPAP---IYTPPPPAPHCPPPPPSAPTPPIPSPPSTLPPPPQAPPNRAPP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FERTILIN ALPHA SUBUNIT.
Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Araijo R., Huizar L., Rowley D., Buehler E., Dunn P.,
Gonzalez A., Kremenetskaia I., Kim C., Lerz C., Li J., Liu S.,
Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
Marker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC011807; AAC13059.1;
InterPro; IPR001561; LRR.
InterPro; IPR002965; P.rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=TESTIS;
Hardy C.M., Holland M.K.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U46069; AAA93320.1; -.
HSSP; P17494; MSST.
MEROPS; M.2.201; -.
INCEFPC; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00019; LEURICHRPT.
PRINTS; PR01217; PRCHEXTENSN.
SMART; SM0370; LRR; 5.
SEQUENCE 494 AA; 54407 MW; BDC0011EEFD5C2E4 CRC64;
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 205; DB 10;
55.1%; Pred. No. 1.1e-08;
tive 5; Mismatches 22;
                                                                                                                                                   494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         919 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                        Created)
                                                                                                                                                     PRT;
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                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                     PRELIMINARY;
                                       ||| ||| | | 484 PPSPPPPPPV 494
                   554 PPSRPPPRPSV 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 PSRPPPRPS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: | |:||
103 PAPPKPQPS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              F14J22.4 PROTEIN.
F14J22.4.
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                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702
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Q28659;
                                                                                                                                                     O9FXA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                             RESULT
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Q28659
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                 815 PPPPFASVRRNSETLLPPPPPPPWKS-----LYASTFETHEACSTSSSPPPPPPP 866
                                                                                                             PPFSPLNTTKANDYILPPPPLPYTSIAPSPSVKILPLHGISSAPSPPVKTAPPPPPPPF 926
                                                                                                                                                                        ---NQPAKY-----PL 497
                                                                                                                                                   NNAYHTSSPPPAPIYTPPPAPHCPPPPPS--APTPPIPSPPS-TLPPPPQAPPNRAPP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 205.5; DB 10; Length 760;
Pred. No. 1.9e-08;
4; Mismatches 20; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pohl T., Weizenegger T., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Robben J., Grymonprez B., Volckaert G, Mewes H.W., Lemcke
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W. Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EV Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049608; CAB40769.1;
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR.out.
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR003862; Pistil_extensin.
Prof0560; LRR; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO1218; PSTLEXTENSIN.
SMART; SM00370; LRR; 4.
SEQUENCE 760 Aa; 82245 MW; 20CDE1C8E6CECFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                       477 DTGRCINFTRVKN--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%;
                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, EXTENSIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                          555 PSRPPPRPS 563
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                                                                                                                                                                                                                                                                983 PPPPPPPS 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Best Local S
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Matches

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Q9TOK5;

RESULT Q9TOK5

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Gaps

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22; Indels

Length 494;

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HISSPPPAP----IYTPPPPAPHC--PPPPPSAPT-----PPIPSPPSTLPPPPQAPPPN 550
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Interpro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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                                                     Ephydroidea; Dra
NCBI_TaxID=7227
CG5514 PROTEIN.
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Best Local Simil
Matches 70; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  614 ----QHTVIQVAY-------EDDWCWSIDSNSGCSDYGDVQRNTYC 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CDSGYAPPDCRNP 701
                                                                                                                                                                                                                                                                                                  511 CSGKSASCPPDAYKQDGTPCDRVYRCLGGQCMNPDKQCSNIYGIPARSAP-----EECYV 565
                                                                                                                                                                                                                                                                                                                        FVEQLAHKF----ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 RKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHC
                                                                                                                                                                                                                                                                                                                                                                    HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAI---VYC
                                                                                                                                                                                                                                                                                                                                                                                                               178 VGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILA----AEPSTICA
                                                                                                                                                                                                                                                                                                                                                                                                                                   649 A-----SCVVYQAPNSDCQADEMCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPA----PILKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 GMKAALQVS-----MNDGLSFISSSVIITTTHCSDG----SILAIALLILFLLLALALLWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 FWPLCCIVIIKEVPPPAEESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEK
                                                                                                                                                                                                                                                                                                                                             LMNSKGDRFGNCGSPPALQSSYVPCADENIFCGKL-----ICTEVKLLPQILP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            797 -PPEQPAQQEAPQQQEAPPAREAPPPE-----AARPAE------
                                                                                                                                                                                                                                    ; Score 204; DB 6; Length 919; Pred. No. 3.4e-08; 68; Mismatches 174; Indels
                                                                                                                                      PROSITE; SM00181; EGF; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50214 DISINTEGRIN_2; 1.
PROSITE; PS001486; EGF_2; UNKNOWN_1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 919 AA; 100844 WW; 32654E431D7CEBAD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                GPCR_Rhodpsn.
Pep_M12B_propep.
Reprolysin.
                                                                      přam; PP00001; 7tm_1; 1.
přam; PP00000; disintegrin; 1.
přam; PP01562; Pep M12B_propep; 1.
přam; PP01421; Reprolysin; 1.
ProDom; PD000664; D18Antegrin; 1.
SMART; SM00050; D1SIN; 1.
                                                           InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity 19.3%;
Matches 113; Conservative 68
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                InterPro; IPR000276;
InterPro; IPR002870;
                                      InterPro; IPR001590;
InterPro; IPR000531;
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01-MAY-2000 (
01-MAY-2000 (
01-JUN-2001 (
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RC STRAIN-BERKELEY;

RA Adams M.D. Celniker S.E. Holt R.A. Evans C.A., Gocayne J.D.,

RA Adams W.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams G.C., Celerer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Bazter E.G., Helt G., Nelson C.R., Malkos G.L.G.,

RA Ballew R.M., Basu A., Barandale J., Bayraktaroglu L., Baldwin D.,

RA Ballew R.M., Basu A., Barandale J., Bayraktaroglu L., Bassley E.M.,

Ballew R.M., Basu D.A., Burler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,

RA Dordon K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann R.,

RA Bordos B., Delebra A., Bownes M., Dugan-Rocha S., Pleischmann R.,

RA Godon K., Doup L.E., Downes M., Dugan P., Harris M.,

Gabriellan A.E., Garyell J.H., Gu Z., Glabar I., Dietz S.M.

RA Godon K., Doup L.E., Downes M., Dugan P., Harris M.,

Gabriellan A.E., Gabriellan A.E., Gary N.S., Gelbart W.M., Classer K.,

RA Godon K., Houston K.A., Howland T.J., Weil M.-H., Ibegwan C.,

RA Harris N.L., Harvey D., Heiman T.J., Weil M.-H., Ibegwan C.,

RA Marmel B.E., Kodirac C.D., Kraft C., Kravit S., Mulp D., Lai Z.,

RA Mettal B., Wolthow B., Wurphy L., Muzny D.M., Nelson D.L.,

RA Reinert K., Remington K.A., Mixon K., Nusskern D., Puri V., Wanger M.,

RA Spier E., Sprading A.C., Stapleton M., Stugeki M.P., Smith T.,

RA Spier E., Sprading S.M., Wolyner E., Wang S., Zhan A., Smith H.O.,

RA Sheng X.H., Zhong F.N., Walley K., Whury D.M., Weissenbach J.,

RA Sheng X.H., Zhong F.N., Walley K., Whury D.M., Weissenbach J.,

RA Godon K., Weisen D., Walley K., Whole K., Shen H.,

RA Sheng X.H., Zhong F.N., Walley M., Walley M., Walley K., Zhon W., Sheng S.
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Ducosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidee; Drosophila.
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27.7%; Pred. No. 5.1e-08;
tive 27; Mismatches 73;
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MEDLINE-97162277; PubMed-9009264;
Godl K., Hallmann A., Wenzl S., Sumper M.;
Lolfferential targetting of closely related ECM-glycoproteins: The pherophorin family from Volvox.";
EMBO J 16:25-34(1997).
EMBL; Y07752; CAA69032.1; -.
                                                                                                                                                                                          Volvox carteri.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBL_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 599;
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6.7%; Score 203; DB 10; Length 59
Best Local Similarity 55.9%; Pred. No. 2.2e-08;
Matches 38; Conservative 1; Mismatches 25; Indels
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8BAA14D5A71F8082 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PHEROPHORIN-S PRECURSOR.
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CHAIN 18 599 PC
SEQUENCE 599 AA; 63436 MW;
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458 KVEPP--PPPAPA 468
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Search completed: August 9, 2002, 10:46:25 Job time: 848 sec

556 SRPPPRPS 563 ||| || 269 PPPPPPS 276

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352 KEVPPP---PAEESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGA 408
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APPLICANT: John, Maliyakal E
APPLICANT: John, Maliyakal E
APPLICANT: Barton, Kenneth A
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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STREET: P.O. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
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ilarity 26.1%; Pred. No. 4.8e-09;
Conservative 18; Mismatches 56
                                               US-08-943-363-37
US-09-193-043-37
US-08-193-043-37
US-08-286-889-2
US-08-485-618-2
US-08-485-618-9
US-08-485-618-9
US-08-485-618-9
US-08-485-618-9
US-08-652-5
US-08-605-672-2
US-08-605-672-2
US-08-482-293A-2
US-08-482-293A-2
US-08-482-293A-9
US-08-943-363-2
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FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATORNEY/AGENT INFORMATION:
NAME: Seay, NICholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11229908;
TELEPHONE: 608-251-500
"TELEPHONE: 608-251-500
"TELEPHONE: GO8-251-9166
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
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Matches 59; Conserv
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Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries

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Maximum DB
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Gaps

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SEQ ID NO:37
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520238-3
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                                                                            PROTEIN
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                                                                                              469 SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPP-- 526
                                                                                                                    109 KLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 PLNNAYHTSSPPPA----PIYTPPP--PAPHCPPP--PPSAPTPPIPSPPSTLPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 186; DB 1; Length 214;
Pred. No. 8.7e-09;
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: John, Mallyakal E
APPLICANT: Barton, Kenneth A
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCES: 16
                                                                                                                                                             527 ---SAPTPPIPSPPSTLPPPP----QAPPPNRAPPP---SRPPPR 561
                                                                                                                                                                                 250 YKYKSPPPPMHSPP---PPTPVXKXKSPPPPMHSPPPVXSPPPPK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,327
                                                               178 -KYKYKSPPPTPVYKYKSPPP-----PTPVYKYKSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
      144 КЅРРРКНЅРАРЕННҮКҮКЅРРРРКНГРАРЕННҮ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
RESISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1122990831
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US-08-217-327-4
Sequence 4, Application US/08217327
Patent No. 5474925
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Quarles and Brady
STREET: P.O. Box 2113
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-500
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 214 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA ZIP: 53701-2113 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 39; Conserva:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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Best Local Si
Matches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 520235

Patent No. 520235

APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,

SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID

IITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
; Patent No. 5202236
; Patent No. 5202236
; Patent Naugh, Kathy J.; ANDERSON, DAVID M.; STRAUSBERG,
; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
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Best Local Similarity 51.6%; Pred. No. 3.1e-07;
Matches 33; Conservative 4; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                              ch
1 Similarity 51.6%; Pred. No. 2.1e-07.
33; Conservative 4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY.1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-MOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                             NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 93,945
FILING DATE: 24-NOV-1886
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
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US-09-080-897-2
; Sequence 2, Application US/09080897
; Patent No. 5985574
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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LENGTH: 334
5202236-3
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Sequence 46, Application US/08286889
Fatent No. 5470953
Fatent No. 5470953
FALTICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 PQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAP--IYTPPPPAPHCPPPPP---- 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.5%; Score 167.5; DB 4; Length 1
35.5%; Pred. No. 4.8e-06;
tive 3; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2IP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/323,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                 FILING DATE:
CLASSTEICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: 09/080,897
FILING DATE:
ATONNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
RELECHONE: (650) 343-4341
TELECHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-323-735-2
    HILLSBOROUGH
                        CALIFORNIA
: USA
                                                                   94010
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US-08-286-889-46
  CITY: HII
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616 TAISPPPLSGDATIPPPPLPEGVGIPSPSSLPGGTAIPPPPPLPGSARIPPP--PPPL 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 -----SAPTPP----IPSPPS----TLPPPQAPPNRAPPPSRPPR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1248;
                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5%; Score 167.5; DB 2;
35.5%; Pred. No. 4.8e-06;
tive 3; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                               ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
                                                                                                       APPLICANT: Leon, Pedro E.

TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELECOMMUNICATION INFORMATION:
TELEPRONE: (650) 343-4341
TELERAX: (650) 343-4341
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09323735
Patent No. 6197932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Loon, Pedro E.
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 35.58
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-080-897-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/08485618
Sequence 46, Application US/08485618
Sequence 5728533
GENERAL INFORMATION:
GAPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
5.5%; Score 166; DB 1;
Best Local Similarity 28.2%; Pred. No. 5.9e-06;
Matches 66; Conservative 42; Mismatches 96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: 312-474-6300
TELECX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acids
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-286-889-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Sequence 46, Application Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 166; DB 1; 28.2%; Pred. No. 5.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
ATTORNEY, ABOUT INFORMATION:
ATTORNEY, AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
FILING DATE: 5-BC-1993
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                   TELBERA: 312-4..
TELERAX: 312-4..
INFORMATION FOR SEQ ID NO: 46: SEQUENC CHARACTERISTICS: SEQUENC CHARACTERISTICS: TENGTH: 1155 amino acids TVPE: amino acid linear inear
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
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Matches 66; Conserv
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CITY: Chicago
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Gaps

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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVF 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | ||: | ||: | | : | | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                     Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                  96; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.5%; Score 166; DB 2; Best Local Similarity 28.2%; Pred. No. 5.9e-06; Matches 66; Conservative 42; Mismatches 96;
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECHONUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFEAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-M0-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATONNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-482-293A-46
Sequence 46, Application US/08482293A
; Patent No. 5831029
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                   US-08-605-672-46
                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Application US/08605672
Patent No. 5817515
ENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                          96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: United States
ZIP: 60060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                        ; Score 166; DB 1;
; Pred. No. 5.9e-06;
42; Mismatches 96
                                                                       27866/32391
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                  NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3
TELEPHONE: 312-474-6300
TELEPA: 312-474-0448
TELER: 25-3856
INFORMATION FOR SED ID NO: 46:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.2%;
Matches 66; Conservative 47
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-362-652-46
                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-08-605-672-46
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Query Match
Best Local Similarity
Matches 66; Conserval
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US-09-193-043-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/08943363
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                             Indels
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APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                    Query Match
5.5%; Score 166; DB 2;
Best Local Similarity 28.2%; Pred. No. 5.9e-06;
Matches 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
APPLICATION NUMBER: 21-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                     27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: 111nois
COUNTRY: United States
ZIP: 66606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27F
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-630
TELEFAX: 312-474-648
                                                                                                    INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 1155 amino acids TYPE: amino acid
                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-482-293A-46
                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-943-363-46
                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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28.2%; Pred. No. 5.9e-06;
tive 42; Mismatches 96;
                                                                                                                                                                                                                                                                                       . 5.5%; Score 166; DB 2;
illarity 28.2%; Pred. No. 5.9e-06;
Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-193-043-66 Application US/09193043
Sequence 46, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6251395e1 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
FARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOUTHWARE: PATENTING DATE: 1997-10-03
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
                                                                       TELERA: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.2%
Matches 66; Conservative
                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Mus musculus
US-09-193-043-46
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LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                 259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
                  149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
CORRESPONDENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                   200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                | : | ||: | | : | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Marshall, O'Toole, Gerstein, Murray & Borun
F: 233 South Wacker Drive, 6300 Sear Tower
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

5.5%; Score 166; DB 1;
Best Local Similarity 28.2%; Pred. No. 5.9e-06;
Matches 66; Conservative 42; Mismatches 96
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CLASSIPECATION: 435
PRIOR APPLICATION: 435
PROF APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
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COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-362-652-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                               US-08-362-652-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                  149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                              259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
AITLE OF INVENTION: NO. 572853381 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                | : | ||: | | :: | | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                   200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.5%; Score 166; DB 1;
28.2%; Pred. No. 5.9e-06;
tive 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            US-08-485-618-53
Sequence 53, Application US/08485618
Fatent No. 5728533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312-474-6300
312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-485-618-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 233 SOI
CITY: Chicago
STATE: Illinoi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Search completed: August 9, 2002, 10:33:08 Job time: 187 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:35:55; Run on:

Search time 98.32 Seconds (without alignments) 525.968 Million cell updates/sec

US-09-970-076-2_COPY_27_321 1536 1 GOGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS 295 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sednence:

528882 segs, 175299045 residues Searched:

528882

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	uo			1823,		ď	24, Appl	20,	194,	301,	26, 4	22,	14,	16,	10,	12,	1170	σ		6, Appli	10,	312,	8,	4	43,	116, App	
	Description	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	•
SUMMARIES	QI QI	PCT-US02-08253-187 (17	-US02-08253-7	7	0-038-307-18	7	0-038-307-24	US-10-038-307-20	PCT-US02-08253-194	PCT-US02-08253-301	US-10-038-307-26	US-10-038-307-22	US-10-038-307-14	0-038-	US-10-038-307-10	US-10-038-307-12	US-09-629-469A-11706	US-10-047-542-99	US-10-104-047-2639	US-10-038-307-6	US-60-373-595-10	7	US-10-038-307-8	US-10-038-307-4	US-09-592-617A-43	PCT-US02-10824-116	
	Length DB	564 1	564 1	564 7	551 6	_	_	564 6	562 1	562 1	328 6	_	<u>-</u>	543 6	_	_	218 5	_	_			587 6	487 6	_	1152 5	1163 1	
æ	Query Match	100.0	100.0	100.0	99.7	99.0	0.66	0.66	98.9	6.86	98.1	98.0	97.7	97.7	97.0	96.3	62.9	58.8	51.5	51.5	51.5	50.6	50.1	44.6	9.5		
	Score	1536	1536	1536	1532	1520	1520	1520	1519	1519	1507	1505.5	1500	1500	1490	1479	996	806	790.5	790.5	790.5	777.5	770		145.5	138.5	
	Result No.	1	7	m	ಶ	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	•

ALIGNMENTS

RESULT	RESULT 1
	-USUZ-UGZD3-IB/ squence 187. Application PC/THSO20833
	DRMATION:
٠.	O
٠.	APPLICANT: St. Croix, Brad
٠.	
۰.	Kinzler, Kenneth
	TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
	FILE REFERENCE: IIO/.OOI/9
	CURRENT FILING DATE: 2002-04-10
	PPLICATION NUME
٠.	PRIOR FILING DATE: 2001-04-11
	PRIOR APPLICATION NUMBER: 60/308,829
٠.	PRIOR FILING DATE: 2001-08-01
	٠
	SOFTWAKE: FastseQ for Windows Version 4.0
	SEQ ID NO TR
	16741n: 004
	1 Ordanism Homo sapiens
3	100.08;
Ma	best bocat similating 100.0%; Fred. NO. 1.28-130; Matches 295; Conservative 0; Mismatches 0; Indels 0; G
οy	1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
qq	27 GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
0y	61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
qq	87 TRGTILMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENROGYRTASVII
Qy	121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
QQ	147 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDENETQLARIADSKDHVFPVNDGFQ
Óγ	181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
q	207 ALGGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
Qy	241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVITTTHCSDGS 295
qq	267 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDGS 321

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Query Match 99.7
Best Local Similarity 100.
Matches 294; Conservative
                                                                          Conservative
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US-10-038-307-18
                                                         Best_Local Similarity
Matches 295; Conserv
US-60-389-987-1823
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Taly, Edin D.
APPLICANT: Taly Bing
APPLICANT: Glbson, Bradford W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnorck, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE REFERENCE: 660088-465P2
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOUTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1823
LENGTH: 564
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                                                                                 APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Brad
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR PLING DATE: 2001-08-01
NUMBER OF SEO ID NOS: 359
SOFTWARE: FastSEO for Windows Version 4.0
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100.0%; Score 1536; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.2e-136;
Matches 295; Conservative 0; Mismatches 0;
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                                                        Sequence 232, Application PC/TUS0208253 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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PCT-US02-08253-232
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LENGTH: 564
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Best Local S
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RESULT 4
US-10-038-307-18
Sequence 18, Application US/10038307
Sequence 18, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTHAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
TILE REPRENENCE: 7553-253-99
CURRENT APPLICATION NUMBER: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 551
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207 ALQGIHHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 266
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                                                     1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                    27 GQGGRREDGGPACYGGPDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 86
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 Length 564;
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100.0%; Pred. No. 2.7e-136;
ive 0; Mismatches 0;
Score 1536; DB 7;
Pred. No. 1.2e-136;
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. The Laley
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
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ORGANISM: Homo sapiens
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US-10-038-307-20
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LENGTH: 564
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                                                                                       APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
KUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.8e-135;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.9e-135;
Matches 292; Conservative 0; Mismatches 0;
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                                                     Sequence 2, Application US/10038307 GENERAL INFORMATION:
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Matches 292; Conservative
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US-10-038-307-24
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TYPE: PRT
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                                                   Gaps
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Length 564;
                                                   Indels
Query Match 99.0%; Score 1520; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 3.8e-135;
Matches 292; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
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; GENERAL INPORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: St. Croix, Brad
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107, 00179
; CURRENT PILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR PELING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 359
; COURTENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: 9C7/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR RILING DATE: 2001-04-11
PRIOR APLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 194
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4.7e-135;
ches 2;
                                                                                                                                                                                                                                                                  Score 1519; DB 1;
Pred. No. 4.7e-135;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1519; DE pred. No. 4.7e-2; Mismatches
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98.6%;
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Best Local Similarity 98.6
Matches 291; Conservative
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                            ; ORGANISM: Mus musculus
PCT-US02-08253-194
                                                                                                                                                                                                                                                                                   Similarity
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Matches 291;
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LENGTH: 562
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1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60

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Sequence 26. Application US/10038307
| Sequence 26. Application US/10038307
| GENERAL INFORMATION:
| APPLICANT: James B. ROTTMAN
| APPLICANT: Theresa L. O'KEEFE
| APPLICANT: Theresa L. O'KEEFE
| APPLICANT: Judith J. HEALEY
| TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
| TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
| TITLE REFERENCE: 7853-253-999
| FILE REFERENCE: 7853-253-999
| CURRENT APPLICANTON NUMBER: US/10/038,307
| CURRENT FILING DATE: 2002-06-28
| NUMBER OF SEQ ID NOS: 26
| SEQ ID NO 26
| SEQ ID NO 26
| LENGTH: 328
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                                                                                                                               ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
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                   84
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                                                       205 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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Pred. No. 3e-134;
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100.0%; Pred. No. c.
... 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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ORGANISM: Homo sapiens
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Matches 290; Conserv
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US-10-038-307-22
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US-10-038-307-26
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James B. FOTTMAN
APPLICANT: James B. O'TKEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TILLE OF INVENTION: Tampo JP and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILLIC DATE IN SOUTH OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASESEQ for Windows Version 4.0
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
  205 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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1larity 98.6%; Pred. No. 2.8e-133;
Conservative 0; Mismatches 2;
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TYPE: PRT

CRGANISM: Homo sapiens

US-10-038-307-16
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Matches 291; Conserv
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                                                                                                                                                                                                                                                                                                                                         Gaps
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APPLICANT: Theresa L. O'KEFE
APPLICANT: Dudith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 543
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                         Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                              1 GQGGRREDGGP-----ACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQ
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                                                                                                                                                                                                                                                                                          Score 1505.5; DB 6
Pred. No. 4.4e-134;
0; Mismatches 0;
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APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
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GENERAL INFORMATION:
APPLICANT: James B. ROTIMAN
                                                                                                                                                                                                                                                                                            Query Match 98.0%;
Best Local Similarity 97.0%;
Matches 292; Conservative
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11; Conservative
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US-10-038-307-22
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Matches 291;
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                                                                                                                                                                   LENGTH: 342
TYPE: PRT
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US-10-038-307-12
Sequence 12, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFF
APPLICANT: Total OSKANNAK
APPLICANT: Modith J. HEALEY
TILE OF INVENTION: Tangon 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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                                                                                                                                                                                                                                                                              27 GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIXYFVEQLAHKFISPQLRMSFIVFS 86
                                                                                                                                                                             Gaps
                                                                                                                                                                                                       1 GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
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                                                                                                                                               Length 543;
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                                                                                                                                                                             3; Indels
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98.3%; Pred. No. 2.6e-131;
tive 0; Mismatches 3;
                                                                                                                                               Ouery Match
Best Local Similarity 98.3%; Pred. No. 2.5e-132;
Matches 290; Conservative 0; Mismatches 3;
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 543
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CRGANISM: Homo sapiens
US-10-038-307-12
                                                                             TYPE: PRT CRGANISM: Homo sapiens US-10-038-307-10
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Best Local Similarity
Matches 288; Conserv
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Search completed: August 9, 2002, 10:35:55 Job time: 353 sec

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Sequence 620, App Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appl Sequence 30, Appli Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 132, Appl Sequence 132, Appl Sequence 132, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 105, Appl Sequence 105, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 59, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 53, Appl Sequence 53, Appl Sequence 57, Appl

4

OM protein

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Sequence:

Fitle:

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APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERRNCE: 960296,97745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2.2
                                                                                                                                                                                                 ALIGNMENTS
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100.0%; Pre
                                                                                                                                                                                                                        ; Sequence 2, Application US/09970076; GENERAL INFORMATION:
                                                                             18
                                                                                   188
                                                                                                                                                                                                                                                                                                          CRGANISM: Homo sapiens US-09-970-076-2
  RESULT 1
US-09-970-076-2
                                                                                                                                                                                                                                                                                                 368
  TYPE: PRT
                                                                                                                                                                                                                                                                                                 LENGTH
  (without alignments)
204.668 Million cell updates/sec
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                                                               GQGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS 295
                                  ; Search time 507.33 Seconds
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                                                                                                                                          Compugen Ltd
                                                                                               hits satisfying chosen parameters:
                                                                                       3502263 seqs, 351980561 residues
     GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                     US-09-970-076-2_COPY_27_321
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Maximum Match 100%
Listing first 45 summaries
                         - protein search, using sw model
                                  August 9, 2002, 10:44:29
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seq length: 2000000000
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Match 1
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Minimum DB Maximum DB

Database

Searched:

16,

Sequence Sequence Sequence

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Gaps

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Length 368; Indels

Score 1536; DB 23; Pred. No. 6.5e-151; Mismatches 0;

Conservative

Query Match Best Local Similarity Matches 295; Conserv

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Sequence 2, Appli Sequence 61, Appl Sequence 621, App Sequence 621, App Sequence 187, App Sequence 232, App Sequence 6, Appli

US-09-970-076-2 PCT-US00-30045-94 PCT-US01-11988-621 US-09-833-245-621 US-09-918-715-187 US-09-918-715-232 US-09-970-076-6

368 403 403 564 564

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RESULT 4
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Best Local Simi
Matches 295;
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                                                      ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
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                                                                                                                                                                                                                                                                                                          APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE REPERENCE: PS708PCT
FILE REPERENCE: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 2000-11-05
PRIOR APPLICATION NUMBER: 2000-105
PRIOR FILING DATE: 2000-06-30
NUMBER FILING DATE: 2000-06-30
SUMMER: PATCHIN VOS: 201
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
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PCT-0501-11988-621
; Sequence 621, Application PC/TUS0111988
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 295; Conservative
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100.0%; Pred. No. 7.4e-151;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                100.0%; Score 1536; DB 1;
100.0%; Pred. No. 7.4e-151;
iive 0; Mismatches 0;
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE:
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
RAIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-31
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER: OF SEQ ID NOS: 2267
SEQ YEAR PARENT PARENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 621, Application US/09833245; GENERAL INFORMATION:
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 35;
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 621
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ORGANISM: Homo sapiens
PCT-US01-11988-621
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9-940-04-60-SD
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TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                              121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
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                                                                                                                                                                                                                                                                                             Sequence 187, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 60/222,599
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SUMBER OF SEQ ID NOS: 358
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100.0%; Pred. No. 1.2e-150;
iive 0; Mismatches 0; 1
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Sequence 232, Application US/09918715
GENERAL INFORMATION:
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Matches 295; Conservative
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181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240
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APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATFERNS
FILE REFERENCE: 1107.00134
CURRENT FILION: 00134
CURRENT FILION DATE: 2001-08-01
PRIOR PLICATION NUMBER: 60/224,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
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GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 960296.9745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 6
LENGTH: 564
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Best Local Similarity 100.
Matches 295; Conservative
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ORGANISM: Homo sapiens
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Xaa equals any of the naturally occurring L-amino acids
RESULT 9
PCT-US01-11988-620
Sequence 620, Application PC/TUS0111988
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FCT
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATCH OF SEQ ID NOS: 2267
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NAME/KEY: SITE
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LENGTH: 403
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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COCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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               ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
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ilarity 99.3%; Pred. No. 1.3e-149;
Conservative 0; Mismatches 2;
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PCT-US00-30045-125
Sequence 125, Application PC/TUS0030045
SERSAL INFORMATION:
REPELICANT: Human Genome Sciences, Inc.
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LOCATION: (175)
OTHER INFORMATION:
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LENGTH: 403
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Xaa equals any of the naturally occurring L-amino acids
                                                Xaa equals any of the naturally occurring L-amino acids
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207 ALOGIIHSILKKSCIEILAAEFSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 266
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llarity 99.3%; Pred. No. 1.3e-149;
Conservative 0; Mismatches 2;
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NO 9
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (368)
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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| GENERAL INFORMATION:
| APPLICANT MILLEUNLUM Pharmaceticals, Inc.
| TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
| TITLE OF INVENTION: ENCODING THEM
| FILE REPRENCE: 7833-173-228
| CURRENT APPLICATION NUMBER: PC/US99/31025
| CURRENT FILING DATE: 1999-12-23
| EARLIER RIPING DATE: 1999-12-33
| EARLIER PILING DATE: 1998-12-36
| CUMBER OF SEO ID NOS: 135
| SOFTWARE: FastSEO for Windows Version 4.0
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Pred. No. 1.3e-149;
0; Mismatches 2;
       GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT

CURRENT APPLICATION NUMBER: US/09/833,245

CURRENT FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PATCHIN OF NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PATCHIN OF 2010-04-25

SEQ ID NO 620
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Best Local Similarity 99.3%;
Matches 293; Conservative (
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PCT-US99-31025-9
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GENERAL INFORMATION:
APPLICANT: HOLTZMAN, DOUGLAS
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 09404/066001
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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100.0%; Pred. No. 2.6e-149;
iive 0; Mismatches 0;
                                                                         Score 1520; DB 1; 1; Pred. No. 2.6e-149; 0; Mismatches 0;
                                                                              99.0%;
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                                                                              Query Match
Best Local Similarity 100.
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-223-546-9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-9
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US-09-796-753-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2. A paplication US/09599596

SEQUENCE A PAPLICANT: Holtzman, Douglas
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 09404/06601
CURRENT APPLICATION NUMBER: US/09/599,596
CURRENT FILING DATE: 2000-06-22
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                            1 GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GOGGRREDGGPACYGGPDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 86
                                                                        APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 333;
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100.0%; Pred. No. 2.6e-149;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         99.0%; Score 1520; DB 18;
ilarity 100.0%; Pred. No. 2.6e-149;
Conservative 0; Mismatches 0;
                                                                                                                                                                                               NUMBER OF SEQ 1D NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.00,
100.0%; Pre
                                     Sequence 9, Application US/09471179 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 292; Conservative
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US-09-599-596-9
                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-471-179-9
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 292; Conserv
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US-09-599-596-9
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                          US-09-471-179-9
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ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240
                                                                                                    ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
                                                                   61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 86
                                                                                                                                                                                                                              207 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McCarthy, Sean A. TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-227-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/99/796,753
CURRENT APPLICATION NUMBER: US/97/83,175
PRIOR APPLICATION NUMBER: US/23,094
PRIOR APPLICATION NUMBER: US/23,094
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR PILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-02-26
PRIOR PILING DATE: 1998-02-26
PRIOR PILING DATE: 1998-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-06-30
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PRIOR PILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 2000-02-25
PRIOR PILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09796753 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                      Length 333;
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| PRIOR FILING DATE: 2000-06-29
| PRIOR APPLICATION NUMBER: 09/606,317
| PRIOR FILING DATE: 2000-06-29
| PRIOR PLICATION NUMBER: 09/65,666
| PRIOR APPLICATION NUMBER: 09/65,666
| PRIOR FILING DATE: 2000-09-20
| PRIOR FILING DATE: 2000-09-30
| NUMBER OF SEQ ID NOS: 162
| SEQ ID NO 12
| LENGTH: 333
| LENGTH: 333
| JENETH OF SEQ ID NOS: 162
| CHORDALISM: HOMO SADIENS
| ORGANISM: HOMO SADIENS
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Search completed: August 9, 2002, 10:44:30 Job time: 868 sec

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                                                                          Sequence 99, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 99, Appl Sequence 1, Appl Sequence 43, Appl Sequence 43, Appl
                                                                                                                                                                     Patent No. 5424399
                                Appli
Appli
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Appli
                                                       , Appl
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
TITLE OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTY: United States
ZIP: 6060-6402
CONTY: United States
ZIP: 6060-6402
COMPITY: HOPPY disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                                                                                                                                                               Sequence 3,
           Sequence
Sequence
Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score 166; DB 1; Length 11
28.2%; Pred. No. 2.8e-09;
.ive 42; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
AURIENT APPLICATION DATA:
AURICATION NUMBER: US/08/286,889
FILING DATE:
         US-08-485-618-2
US-08-485-618-9
US-08-485-618-99
US-08-605-672-2
US-08-605-672-99
US-08-605-672-99
US-08-482-293A-99
US-08-943-363-99
US-08-943-363-99
US-09-193-043-2
US-09-193-043-99
US-09-193-043-99
US-08-476-062A-43
                                                                                                                                                                             US-08-173-497-3
US-08-286-889-3
                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 23-DEC-1993
ATTORNEY-AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P98,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                     5424399-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                ; Sequence 46, Application US/08286889; Patent No. 5470953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELGEAX: 312-4/2
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
"PWGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.8
Best Local Similarity 28.2
Matches 66; Conservative
 ) MOLECULE TYPE: protein US-08-286-889-46
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  TOPOLOGY:
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US-08-286-889-46
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                                                                                      (without alignments)
158.433 Million cell updates/sec
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Sequence 46,
Sequence 46,
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                                                                            ; Search time 45.48 Seconds
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1 GQGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS
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/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/APCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                       Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08 485-618-46
US-08 362-652-46
US-08 892-534-46
US-08 942-293A-46
US-08 943-363-46
US-09 193-043-46
US-08 1485-618-53
US-08 1485-618-53
US-08 1485-618-53
US-08 1485-618-53
US-08 1485-618-37
US-08 1485-137
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US-08-943-363-55
US-09-193-043-55
US-08-173-497-2
                                                                                                                                                                                                                          hits satisfying chosen parameters:
          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                     231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                         us-09-970-076-2_COPY_27_32
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    protein search, using sw model

                                                                            9, 2002, 10:33:03
                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                              August
                                                                                                                                                                                                                           Fotal number of
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Perfect score:
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                                                                                                                                                                    Scoring table:
                                                       OM protein
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LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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                                                                                                                                             69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
                                                                 204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                    TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, Orlois, Gerstein, Murray & Borun
144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSFSLMQYSNILKTHFT
                                                                                                                                                                                                    174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                  Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
STATE: United States
COUNTY: United States
ZIP: 6060-6402
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PROPERING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NAMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 166; DB 1; 28.2%; Pred. No. 2.8e-09; tive 42; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 23-DEC-1993
FRICH APPLICATION DATA:
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application US/08362652 Patent No. 5766850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312-474-0448
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Best Local Similarity
Matches 66; Conserva
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                                                                                                                                                                                                                                                                                                                                     US-08-362-652-46
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                                                                                                         123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                   69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
                     2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                    10.8%; Score 166; DB 1; Length 1155; 28.2%; Pred. No. 2.8e-09; ive 42; Mismatches 96; Indels 3
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485,618
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/08485618
Sequence 46, Application US/08485618
Patent No. 5228533
Patent LINFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
ITILE OF INVENTION: No. 5728533el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27866/32797
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Illinois COUNTRY: United States ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPASSIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 46:
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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Best Local S
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123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                  69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                             174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                          | : | | | : | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 166; DB 2; 28.2%; Pred. No. 2.8e-09; iive 42; Mismatches 96
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTONREY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                      Sequence 46, Application US/08482293A Patent No. 5831029 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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Matches 66; Conservative
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                                                                                                                                                                                                                             RESULT 5
US-08-482-293A-46
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                                                                       144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                             123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                     174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                             | : | | : | | : | | : | | 316 KVGN-FVALKSIQRQIQEK---IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 166; DB 2;
; Pred. No. 2.8e-09;
42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/173,497
FILING DATE: 2-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAMME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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APPLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                                                                                                                                                                                                 US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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28.2%;
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312-474-0448
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Best Local Similarity 28.2%
Matches 66; Conservative
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COUNTRY: United States
ZIP: 60606-6402
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; ORGANISM: Mus musculus US-09-193-043-46
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Best Local Similarity
Matches 66; Conserva
                                                                                                                                              RESULT 7
US-09-193-043-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                       11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                                                                                                                                                                                                   Sequence.
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vor Sex Vicren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 166; DB 2;
; Pred. No. 2.8e-09;
42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                         Sequence 46, Application US/08943363
Patent No. 5837478
                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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28.2%;
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Best Local Similarity 28.29
Matches 66; Conservative
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3Y: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                             RESULT 6
US-08-943-363-46
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APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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                                                                   174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                Score 166; DB 4; Length 1155;
Pred. No. 2.8e-09;
2; Mismatches 96; Indels 3
                                                                                                                                                                                                                   Sequence 46, Application US/09193043
; Sequence 46, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION;
; APPLICANT: Gallatin, Michael N.
; APPLICANT: Gallatin, Michael N.
; TITLE OF INVENTION: NO. 6251395el Human 2
FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; CURRENT FILING DATE: 1993-12-23
; EARLIER FILING DATE: 1993-12-23
; EARLIER FILING DATE: 1994-08-05
; EARLIER PLING DATE: 1994-08-05
; EARLIER FILING DATE: 1997-10-03
; NUMBER: OF SEQ DI NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-485-618-53
Squence 53, Application US/08485618
Patent No. 5728533
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28.2%;
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CITY: Chlosgo
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
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69 LTEDR-----EQIROGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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Sequence 53, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 581751561 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                    PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                       FILING DATE:

CLASSIFICATION: 435

RIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRICA APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 38,659

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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                                      COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
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      MEDIUM TYPE:
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Sequence 53, Application US/08362652

Sequence 53, Application US/08362652

Sequence 53, Application US/08362652

Sexence 53, Application US/0836262

Sexence No. Sequence 53, Application W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTON: NO. 5766850el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: MATSHALL, O'TOOLe, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 166; DB 1; Length 1161; 28.2%; Pred. No. 2.9e-09;
                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Mismatches
                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY-AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3279;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27866/32797
                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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      COMPUTER READABLE FORM:
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Matches 66; Conserw
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123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
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Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van dar Vieren, Monica
APPLICANT: Van dar Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.8%; Score 166; DB 2; Length 1161; Best Local Similarity 28.2%; Pred. No. 2.9e-09; Matches 66; Conservative 42; Mismatches 96; Indels 30
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                        FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAMME: Williams Jr., JOSEPH A.
NAMME: Williams Jr., JOSEPH A.
NAMME: WIlliams Jr., JOSEPH A.
NAMME: WIlliams Jr., JOSEPH A.
NAMME: WILLIAMS JR., JOSEPH A.
NAMME: WILLIAMS JR., JOSEPH A.
NAMME: WILLIAMS JR., JOSEPH A.
NAMME: WILLIAMS JR., JOSEPH A.
NAMME: WILLIAMS JR., JOSEPH A.
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NAMME: WILLIAMS JR., JOSEPH A.
NAMME: WILLIAMS JR., JOSEPH A.
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APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
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LENGTH: 1161 amino acids
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APPLICATION NUMBER: US
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US-08-943-363-53
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; Pred. No. 2.9e-09;
42; Mismatches 96; Indels 30
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Sequence 33. Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-6402
COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                 CURENT APPLICATION DATA:
CURSENI PATE:
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE:
23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEFRAN: 312-474-6300
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28.2%;
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LENGTH: 1161 amino acids
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COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Watch 10.8%
Best Local Similarity 28.2%
Matches 66; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-605-672-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
CORRESPONDENCE: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | | : | | : | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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10.4%; Score 159.5; DB 1; Length 1151;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
Matches 63; Conservative 41; Mismatches 93; Indels 29;
                                                                                          Length 1161;
                                                                                     10.8%; Score 166; DB 4; Length 116
28.2%; Pred. No. 2.9e-09;
tive 42; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 233 SOUTH Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: 111nois COUNTRY: United States 21P: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTONREY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
FEGINAL PARTICE NUMBER: 27866/32168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/08286889 Patent No. 5470953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
                                                                                                                                         66; Conservative
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MOLECULE TYPE: protein

US-08-286-889-37
; ORGANISM: Mus musculus US-09-193-043-53
                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-08-286-889-37
                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%; Score 166; DB 2; Length 1161; 28.2%; Pred. No. 2.9e-09; tive 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6251395el Human 2
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1994-08-05
EARLIER PPLICATION NUMBER: 08/362,652
EARLIER PILING DATE: 1994-12-21
EARLIER PLING DATE: 1994-12-21
EARLIER PILING DATE: 1997-10-03
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTONEY,AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-474-6300
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; Sequence 53, Application US/09193043
; Patent No. 6251395
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-943-363-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                        CLASSIFICATION:
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TOPOLOGY:
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Squence 37, Application US/08485618
Facent No. 5728533
GENERAL INFORMATION:
FAPTLCANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVEWION:
No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COMPUTRY: United States
ZIP: 6060-6402
COMPUTRY: United States
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                                                                                                                                                                                                                                 131 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 181
18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE---- 71
                                                                                                                                                                            72 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
                                                    29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 LRSIQRQLQEK----IFALEGTQSRSSSSFQHEMSQEGFSSALTSD 354
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OURRENT APLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:
CLASSIFICATION NATA:

APPLICATION NUMBER: US/08/13,497

FILING DATE:
APPLICATION NUMBER: US 08/173,497

FILING DATE: 33-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-40G-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652

FILING DATE: 1-DEC-1994

ATTORNEY/AGENT INFORMATION:
NAME: Williams U: Joseph A.

RESISTATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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ilarity 27.9%; Pred. No. 1.5e-08;
Conservative 41; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
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LENGTH: 1151 amino acids
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Matches 63; Conserva
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US-08-485-618-37
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2002, 10:34:12; Search time 61.73 Seconds (without alignments) 459.199 Million cell updates/sec August Run on:

US-09-970-076-2_COPY_27_321 1536 1 GGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS 295 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283138 283138 seqs, 96089334 residues

Searched:

hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_71:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cell surface glyco	surface	ager	leukocyte surface		collagen alpha 1(X	immunodominant mic	classical-compleme	collagen alpha 1(X		hypothetical prote	type XII collagen	cartilage matrix p	complement factor	collagen alpha 1(V	complement factor	collagen alpha 2(V	cartilage matrix p	cartilage matrix p	hypothetical prote	complement factor	sporozoite surface	hypothetical prote		thrombospondin-rel	dnaK protein (heat	like pr	alph	alpha
ID	RWHU1B	RWHU1C	A40020	800551	A48569 .	A45974	A45638	C2MS	S31212	S78476	S42373	151027	A37979	ввни	A54849	BBMS	S21369	S66522	A33809	T28797	151579	A46283	T23087	S33578	S04531 .	B96958	T50240	S09646	CGHU2A
DB	: -	Н	Н	7	~	-	~	Н	~	7	~	7	7	-	~	٦	٦	7	~	~	~	~	~	N	~	7	7	7	Н
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% Query Match	9.5	9.3	•	•	9.0	8 6.8	٠.	8.5	•	8.5	8.3	7.7	7.4	7.4	7.3	7.2	7.1	7.1		6.9		•	6.5	6.5	6.4	6.4	6.4	6.4	6.4
Score	145.5	4	143	141	139	137	134.5	131	130	130	128	118	113.5	113.5	111.5	110.5	109.5	108.5	107.5	105.5	104	100.5	100	99.5	66	66	66	66	66
Result No.		7	m	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

hypothetical prote	hypothetical prote	collagen alpha 3(V	dnaK protein NMB05	collagen alpha 3(V	hypothetical prote	integrin alpha-1 -	probable retroelem	transcription regu	inter-alpha-inhibi	integrin alpha-E c	integrin alpha-1 c	undulin 1 - human	hypothetical prote	probable chaperone	transposase (04) B
T04822	T46488	CGHU3A	н81185	A37797	T47637	A55348	F84811	AF1166	JC5953	A53213	A45226	A40970	E70121	B81917	B83736
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98.5 6.4	_		97.5 6		96.5 6	9 96	9 96			95.5 6.				92.5 6	

Our Surface glycoprotein CD11b precursor [validated] - human
N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein
eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2000
C;Accession: A31108; A28915; A41600; A30892; A3218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3,

A; Reference number: A31108; MUID:88315033

A; Accession: A31108
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Cross-references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: part of this sequence was confirmed by protein sequencing
A; Annaout, M.A.; Gupta, S.K.; Plerce, M.W.; Tenen, D.G.
J. Cell Blol. 106, 2153-2158, 1988
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion recepto
A; Reference number: A28915; MUID:88257215
A; Recession: A28915

A Molecule type: mRNA
A; Residues: 1-499, 501-965, 'P', 967-1153 < ARN>
A; Residues: 1-499, 501-965, 'P', 967-1153 < ARN>
A; Residues: 1-499, 501-965, 'P', 967-1153 < ARN>
A; Cross-references: GB:MI8044; GB:J03270; GB:MI9664; GB:X07421; NID:g186935; PIDN:AAA
A; Note: the authors translated the codon TAC for residue 1129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was con
B; Shellaley, C.S.; Arnaout, MA.
B; Shellaley, C.S.; Arnaout, MA.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Title: The promoter of the CD11b gene directs myeloid-specific and developmentally
A; Reference number: A41600; MUID:92073318

A.Accession: A41600
A.Accession: A41600
A.Accession: A41600
A.Accession: A41600
A.Accession: A41600
A.Accession: A30892
B.Accession: A30892
A.Accession: A30892

A; Wolecule type: mRNA
A; Residues: 917-1042 <AR2>
A; Residues: 917-1042 <AR2>
A; Residues: 917-1042 <AR2>
A; Residues: 917-1042 <AR2>
B; Rickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A; Title: cDNA sequence for the alpham subunit of the human neutrophil adherence recep A; Areference number: A32218; MUID:89098893
A; Accession: A32218

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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Query Match
Best Local Similarity 24.8
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-834 <CO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A35543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
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A; Note: part of this sequence was confirmed by protein sequencing
R; Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
A; Reference number: A46526; MUID:93123748
A; Recession: A46526
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-499; 501-1153 <FLE>
A; Residues: 1-499; 501-1153 <FLE>
A; Residues: 1-499; 501-1153 <FLE>
A; Residues: Biss5227; NID:9263047; PIDN:AAB24821.1; PID:9263049
A; Cross-references: GB:S5227; NID: Biss5227; NID: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GUB:1TGAW; CKAA
A;Gene: GUB:1TGAW; CKAA
A;Cross-references: GDB:120599; OMIN:120980
A;ATOSS-references: GDB:12-16p11.2
A;Note: promoter contains a GAFA motif and two Spl consensus binding sites
A;Note: promoter contains a GAFA motif and two Spl consensus binding sites
A;Note: promoter contains a GAFA motif and two Spl consensus binding sites
A;Note: promoter cells urface glycoprotein CDlib; von Willebrand factor type A repeat home
C;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein for heterodimer; mag
C;Keywords: alternative splicing; calcium factors predicted CEXT>
F;17-1169/Domain: extracellular *status predicted CEXT>
F;17-1108/Domain: calcium/magnesium binding *status predicted
F;530-6514/Region: calcium/magnesium binding *status predicted
F;530-661/Region: calcium/magnesium binding *status predicted
F;51109-1134/Domain: thrracellular *status predicted CITM>
F;1135-1153/Domain: thrracellular *status predicted CITM>
F;1135-1153/Domain: thrracellular *status predicted CITM>
F;86,240,391,469,693,697,735,802,881,901,912,941,979,994,1022,1045,1051,1076/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 FTFKEFONNPNPRSLYKPIIQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR-----IADS--KDHVFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 DGEKFGDPLGYEDVIPEADRE---GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFO 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED---- 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Characterization of the myeloid-specific CD11b promoter. A, Reference number: 152567; MUID:92144986
A, Accession: 152567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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R; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-9 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: protein
Residues: 17-31 <PIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 60; Conserv
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RESULT RWHU1C

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A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:11-2-16p11.2
A; Map position: 16p11.2-16p11.2
C; Superfamily: cell surface glycoprotein CDIlb; von Willebrand factor type A repeat h C; Superfamily: cell surface glycoprotein GDIC #status predicted cSIG> F; 1-19-7Domain: signal sequence #status predicted cSIG> F; 20-1107/Domain: extracellular #status predicted cRIX>
F; 20-1107/Domain: willebrand factor type A repeat homology cVWA4> F; 1108-1137/Domain: transmembrane #status predicted cTMM> F; 1108-1137/Domain: intracellular #status predicted cINT> F; 1134-11637/Domain: intracellular #status predicted cINT> F; 1134-11637/Domain: intracellular #status predicted cINT> F; 1184-11637/Domain: intracellular #status predicted cINT> F; 61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn). (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A35584
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1163 COR>
A; Note: this revision to the sequence from reference A35543 includes the carboxyl end
A; Note: this revision to the sequence from reference A35543 includes the carboxyl end
B; Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
T; Bold: Chem. 265, 2782-2788, 1990
A; Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecu
A; Reference number: A35543; MUID:90153906
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chicken N;Alternate names: fibrochimerin C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revision 10-Sep-1999 #sequence_revis
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cell surface glycoprotein CDIIc precursor - human
NyAlternate names: leukocyte adhesion receptor p150,95 alpha chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A35844; A35543; S00864
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R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer,
EMBO J. 6, 4023-4028, 1987
A;Title: cDNA cloning and complete primary structure of the alpha s
A;Reference number: $00864; MUID:88166645
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; Pred. No. 0.0021;
43; Mismatches 89;
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                                                                                                                                                                                                                                                                                                                                        R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A. J. Biol. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
A;Contents: erratum
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A. Cross-references: GB:M81695; EMBL:Y00093:
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leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
N;Alternate names: complement-3 receptor alpha chain
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S00551; 159078
R;Pytela, R.
EMBO J. 7, 1371-1378, 1988
EMBO J. 7, 1371-1378, 1988
A;Fitle: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Reference number: S00551; MUID:88312584
A;Accession: S00551
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A; Residues: 1-1153 <PTY-
A; Residues: 1-1153 <PTY-
A; Crossreferences: EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A; Crossreferences: EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A; Note: the authors translated the codon CAC for residue 569 as Gln
R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Rober
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement re
A; Accession: 159078
A; Accession: 159078
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A;Molecule type: DNA
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A.Introns: 2845/3; 2867/3; 2889/3; 2922/1; 2885/1; 3008/1; 3065/1
C.(Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von Wi
C.(Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von Wi
C.(Seywords: alternative splicing: cell binding; colled coll; connective tissue; disulfid
C.(Seywords: alternative splicing: cell binding; colled coll;
C.) 23/Domain: signal sequence #status predicted <SIG>
F; 2-23/Domain: signal sequence #status predicted <SIG>
F; 24.1189-3134/Product: collagen alpha 1(XII) chain short splice form #status predicted
F; 24.1189-3134/Product: collagen alpha 1(XII) chain short splice form #status predicted
F; 24.1180-3134/Product: collagen alpha 1(XII) chain short splice form #status predicted
F; 34.1180-3134/Productin type III repeat homology <FN3B>
F; 332-444/Domain: fibronectin type III repeat homology <FN3B>
F; 629-1178/Domain: fibronectin type III repeat homology <FN3C>
F; 629-1178/Domain: fibronectin type III repeat homology <FN3E>
F; 905-986/Domain: fibronectin type III repeat homology <FN3E>
F; 905-986/Domain: fibronectin type III repeat homology <FN3E>
F; 995-1076/Domain: fibronectin type III repeat homology <FN3E>
FY 905-908/Domain: fibronectin type III repeat homology <FN3E>
FY 905-908/Domain: fibronectin type III repeat homo
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: MRNA
A; Residues: 1-3124 «YAM>
A; Residues: 1-3124 «YAM>
A; Residues: 1-3124 «YAM>
A; Cross-references: GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A; Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and, A; Cross-references: GB:D00824; NID:g0.
B; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J: Biol. Chem. 264, 19772-1978, 1989
A; Title: Type XII collagen. A large multidomain molecule with partial homology to type I A; Reference number: A34485, MUD:90062079
A; Residues: 2456-2758 A; A'.2760-2802, F', 2804-2976, F', 2978-3124 <GGR>
A; Molecule type: mRNA
A; Residues: 2456-2788 A; A'.2760-2802, F', 2804-2976, F', 2978-3124 <GGR>
A; Molecule type: protein
A; Residues: 2772-2792; 2846-2873 <GGR2>
A; Molecule type: protein
A; Residues: 2772-2792; 2846-2873 <GGR2>
A; Molecule type: protein
A; Residues: 2772-2792; 2846-2873 <GR2>
A; Molecule type: MUD:87317590
A; Title: Type XII collagen: distinct extracellular matrix component discovered by CDNA CA; Reference number: A28037; MUD:87317590
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A; Molecule type: protein
A; Molecule type: protein
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B; Molecule type: protein
A; Molecule type: protein
B; Molecule type: protein
A; Molecule type: protein
B; Molecule type: prote
           C;Accession: A40020; A34485; B34485; A28037; S22814; S22254; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obax
J. Cell Biol. I15, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule we nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A;Reference number: A40020; MUID:92011862
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A; Residues: 2960-2976, Fr, 2978-3074, 'AG' <GOR3>
A; Cross-references: EMBL:M17375; NID:9211649; PIDN:AAA48718.1; PID:9211650
A; Note: this sequence has been revised in reference A34485
R; Koch, M; Bernascont, C.; Chiquet, M.
Bur. J. Biochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel large form a A; Reference number: S23814; MUID:92362621
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A;Residues: 2811-2832, Tr, 2834, 'R', 2836-2843;3002-3014 <DUB>

A;Residues: 2811-2822, Tr, 2834, 'R', 2836-2843;3002-3014 <DUB>

R;Trueb, J.; Trueb, B.

Biochim. Biophys. Acta 1171, 97-98, 1992

Biochim. Biophys. Acta 1171, 97-98, 1992

A;Title: The two splice variants of collagen XII share a common 5'A;Reference number: $28811; MUID:93042014

A;Accession: $228811
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A;Molecule type: mRNA
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
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A; Accession: 3-vores.
A; Accession: 3-vores.
A; Residues: 1472-1660 (APT>
A; Residues: 1472-1660 (APT>
A; Residues: 1472-1660 (APT>
A; Residues: BMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175
A; Cross-references: EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175
A; Trueb, J.: Trueb, B.
Bur. J. Biochem. 207, 549-557, 1992
A; Reference number: $22916; MUID:92339443
A; Reference number: $22916; MUID:92339443
A; Residues: Preliminary
A; Molecule type: mRNA
A; Residues: 286-494, Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 (-TRU)
A; Residues: 286-494, Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439
A; Residues: 286-494, Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439
A; Residues: 201, 333-338, 1991
A; Title: Cloning of a cDNA for a new member of the class of fibril-associated collage
A; Reference number: $17035; MUID:92037585
A; Molecule type: mRNA
A; Residues: 1472-1659
A; Residues: 1472-1659
A; Residues: 1472-1659
A; Residues: 1472-1659
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A45974; 330085; S22916; S17035; S20833
E;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.;
J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. Experimental Source: embryo skin A. Note: sequence inconsistent with the nucleotide translation A. Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365) A. Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365) B. A. Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365) B. A. Note: sequence number: S30085
A. Accession: S30085
SDSRAQNADLLAAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVWTDG
                                                                                                                        161 A-----SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPR
                                                                                126 ELHEDLFFYSERE-----ANRSRDLGALVYCVGV-KDFNETQLARIA--DSKDHV-FP-
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A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken
                                                                                                                                                                                                                                     175 -VNDGFQALQGIIHSILKKSCIEI----LAAEPSTI--CAGE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137; DB 1;
No. 0.012;
                                                                                                                                                                                                                                                                                     213 YLQSNWGGVSSQINGIIKAACKDLAKDAVCSEWSEYGPCEGE
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A;Accession: A45974
A;Status: preliminary
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A; Residues: 1-1747 <GER>
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R; Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
R; Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
Mol. Biochem. Parasitol. 57, 171-174, 1993
Mol. Biochem. Parasitol. 57, 171-174, 1993
Mol. Biochem. Parasitol. 57, 171-174, 1993
A; Title: Sequence of a major Eineria maxima antigen homologous to the Eineria tenella mi
A; Recession: A48569
A; Accession: A48569
A; Status: preliminary
A; Molecule type: nucleic acid
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C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 234
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                                                                    A; Residues: 11-44 <RES>
A; Cross-references: GB:M14293; NID:9198993; PIDN:AAA39484.1; PID:9554193
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26.6%; Pred. No. 0.0026;
iive 40; Mismatches 89;
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356 -SASITSN-----
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23.2%; Pred. No. 0.012;
Live 56; Mismatches 115;
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"328-296/Domain: thrombospondin type I repeat homology CTHRI>
"5309-371/Domain: thrombospondin type I repeat homology cTHRI>
"5309-371/Domain: thrombospondin type I repeat homology CTHRI>
"5109-371/Domain: thrombospondin type I repeat homology CTHRI>
"5131-493/Domain: thrombospondin type I repeat homology CTHRI>
"5100-371/Domain: thrombospondin type I repeat homology CTHRI>
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C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A45638
R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
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                                Gaps
                                                                                                              DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 71
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A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064
A;Accession: A45638
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24.6%; Pred. No. 0.0059;
tive 40; Mismatches 88;
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                           45;
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A) Note: sequence ext.
C) Superfamily: throw
F) 238-296/Domain: to
F) 238-296/Domain: ti
F; 309-371/Domain: ti
F; 372-432/Domain: ti
F; 433-493/Domain: ti
F; 443-495/Domain: ti
F; 443-495/Domain: ti
F; 449-56/Domain: ti
F; 560-610/Domain: ti
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A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146
C;Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronecti
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A; Gene: Coll4Al

C; Superfamily: collagen alpha 1(XIV) chain; fibronectin type III repeat homology; won C; Superfamily: collagen alpha 1(XIV) chain; extracellular matrix; glycoprotein; tr C; Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; tr; 1-28/Domain: signal sequence #status predicted <SIG>
F; 29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F; 29-100 Commain: fibronectin type III repeat homology <RN3A>
F; 32-433/Domain: fibronectin type III repeat homology <RN3B>
F; 34-614/Domain: fibronectin type III repeat homology <RN3E>
F; 33-707/Domain: fibronectin type III repeat homology <RN3E>
F; 33-404/Domain: fibronectin type III repeat homology <RN3E>
F; 33-404/Domain: fibronectin type III repeat homology <RN3E>
F; 32-1009/Domain: fibronectin type III repeat homology <RN3E>
F; 922-1009/Domain: fibronectin type III repeat homology <RN3E>
F; 922-1009/Domain: fibronectin type III repeat homology <RN3E>
F; 1040-1205/Domain: fibronectin type III repeat homology <RN3E>
F; 1040-1205/Domain: fibronectin type III repeat homology </ri>
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hypothetical protein T20G5.3 - Caenorhabditis elegans
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                                                                                                                                                   18 DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 71
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Pred. No. 0.05;
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A; Residues: 1-416;1460-1811,1843-1888 <WAE>
A; Cross-references: EMBL:X70793
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A; Reference number: S78476
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Matches 62; Conserv
                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1888 <TRU>
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A; Recented acid sequence not shown; translation not shown
A; Accession: 331212
A; Recenter acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-1857 WARA
A; Residues: 1-1857 WARA
A; Residues: 1-1857 WARA
A; Residues: 1-1857 WARA
A; Residues: EMBL:X70792; NID:9288874; PIDN:CAA50063.1; PID:9288875
A; Cross-references: EMBL:X70792; NID:9288874; PIDN:CAA50063.1; PID:9288875
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C; Generics:
A; Gene: Coll4A1
C; Superfamily: collagen alpha 1(XIV) chain; fibronectin type III repeat homology chans
E; 29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted cMAT>
F; 29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted cMAT>
F; 29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted cMAT>
F; 29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted cMAT>
F; 39-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted cMAT>
F; 39-1857/Promain: fibronectin type III repeat homology cFN35>
F; 34-614/Domain: fibronectin type III repeat homology cFN35>
F; 322-1009/Domain: fibronectin type III repeat homology cFN35>
F; 222-1009/Domain: fibronectin type III repeat homology cFN35>
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
C;Accession: 878476; S31211
Submitted to the EMBL Data Library, January 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(XIV) chain precursor, short form - chicken c; Species: Gallus gallus (chicken) C; Species: Gallus gallus (chicken) C; Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
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R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb,
Eur. J. Blochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668
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; Pred. No. 0.049;
44; Mismatches 116; Indels 2
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ilarity 25.0%;
Conservative 44
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cartilage matrix protein precursor - human
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A; Residues: 1-496 <JEN>
A; Cross-references: GB:J05667
A; Accession: B37979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C;Accession: 151027
R:Wel, Y:; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII collag A; Reference number: 151027; MUID:95246925
A;Status: preliminary; translated for a contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th
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C;Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von
F;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP 245
                                                                                                                                                                                                                                                                                                                                                                             ||||||| CYGGEVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVFKNEVLRFVREFV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                       -----DLYFILDKSGSVLHH--WNEIYYFVEQLA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 203
       homology <VWAl> <2F1>
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                                                                                                                                                                                   Length 3051;
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                                                                                                                                                                                                                                                               Indels
F;512-679/Domain: von Willebrand factor type A repeat F;754-793/Domain: fibronectin type II repeat homology F;1201-1244/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                               75;
                                                                                                                                                                                      Score 128; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-929 <WEI>
                                                                                                                                                                                   Query Match 8.3%; Score 128; DB 2
Best Local Similarity 27.1%; Pred. No. 0.14;
Matches 64; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 FSVEDTYLLCPAPILKEVGMKAALQVSMN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: |: |: |: 862 ---QEVYVRGTQTTTVLVGLKPETEYYVN 887
                                                                                                                                                                                                                                                                                                                                   13 CYGGF----
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RESULT A37979

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Definition of factor B precursor [validated] - human

Complement factor B precursor [validated] - human

N.Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; he

N.Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; he

N.Alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragmen

C; Species: Homo Sapiens (man)

C; Date: 19-Feb-1984 #sequence_revision 0.5-Aug-1994 #text_change 08-Dec-2000

C; Date: 19-Feb-1984 #sequence_revision 0.5-Aug-1994 #text_change 0.8-Dec-2000

C; Date: 19-Feb-1984 #sequence_revision 0.5-Aug-1994 #text_change 0.8-Dec-2000

C; Date: 19-Feb-1984 #sequence_revision 0.5-Aug-1994 #text_change 0.8-Dec-2000

A; Reference number: S34075

A; Rodds, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R.

Proc. Natl. Acad Sci. Us.A. 79, 5661-5665, 1982

A; Title: Isolation of cDNA clones for the human complement protein factor B, a class A; Reference number: A44622; MUID:83039428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Map position: 1935-1935
A; Introns: 32/1; 147/3; 22/1; 264/1; 403/1; 454/1; 481/1
C; Complex: homotrimer
C; Complex: homotrimer
C; Superfamily: unassigned EGF-related proteins; EGF homology; von Willebrand factor t
C; Keywords: glycoprotein; homotrimer
F; 1-22/Domain: signal sequence **status predicted <SIG>
F; 1-22/Domain: signal sequence **status predicted <AMT>
F; 23-496/Product: cartilage matrix protein **status predicted <AMT>
F; 23-496/Domain: von Willebrand factor type A repeat homology <VWA1>
F; 27-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F; 75: 344/Ahinding site: carbohydrate (Asn) (covalent) **status predicted
F; 221-238, 234-247, 249-262/Disulfide bonds: **status predicted
C;Species: Homo sapiens (man)
C;Species: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Date: 137-Jul-1991 #sequence_revision 12-Jul-1991 #.K.; Eddy Jr., R.L.; Byers, M.G.; K;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matr A;Reference number: A37979; MUID:91060568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 --VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS--KDHVF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----YENRQGYRTAS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 CYGG-----FDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMSFIV---FSTR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Gene: GDB:CRTM
A)Cross-references: GDB:127280; OMIM:115437
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A.Pathway: complement alternate pathway
A.Pathway: complement C2; complement factor H repeat homology; trypsin homology;
C.Superfamily: complement C2; complement alternate pathway; duplication; glycoprotein; hyd
C.Superfamily: source phase; complement alternate pathway; duplication; glycoprotein; hyd
F; 12-57.Domain: signal sequence #status predicted <SIG>
F; 12-57.Domain: signal sequence #status experimental <BAF>
F; 26-759.Product: complement factor B #status experimental <BAF>
F; 103-158.Domain: complement factor H repeat homology <FH12>
F; 103-158.Domain: complement factor H repeat homology <FH2>
F; 165-218.Domain: complement factor H repeat homology <FH3>
F; 268-458.Domain: complement factor H repeat homology <FH3>
F; 268-458.Domain: von Millebrand factor type A repeat homology <VFA>
F; 482-752.Domain: von Millebrand factor type A repeat homology <VFA>
F; 310-76, 52-98, 103-145, 131-158, 165-205, 191-218, 478-596, 511-527, 599-615, 656-682, 695-725
F; 122, 142, 285, 378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 256-50/Cleavage site: Arg-Lys (complement factor D) #status experimental
F; 256, 576, 699/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                               A, Cross references: GDB:119726; OMIM:138470
A; Cross references: GDB:119726; OMIM:138470
A; Map position: 6p21.3-6p21.3
A; Map position: 6p21.3-6p21.3
A; Map position: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A; Mitrons: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 54/1; 593/2; 619/1; 652/3; A; Mote: the list of introns may be incompletely complex, class III region A; Note: gene is located in the major histocompatibility complex, class III region C; Complex: complement factor B initially forms an inactive complex with complement factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(VII) chain precursor - human N;Alternate names: procollagen alpha 1(VII) chain N;Alternate names: procollagen alpha 1(VII) chain C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: Asquence_revision 04-Nov-1994 #text_change 20-Sep-1999 C;Accession: A54649; PH0844; S16316; 156328; A30296; I84686 R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Ultto, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FERASEQIYYENR-----QGY-RTASVIIALTDG-------ELHEDLFFYSE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REANRSRDLGALVYCVG--VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 194
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-31, 'Q', '33-764 <RE2>
A;Cross-references: GB:LL5702; NID:g291921; PIDN:AAA16820.1; PID:g291922
C;Comment: 292-Cys has a free sulfhydryl.
C;Genetics:
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19.6%; Pred. No. 0.34;
tive 63; Mismatches 109;
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A;Molecule type: mRNA
A;Residues: 16-225, F', 227-259 <MOR>
A;Residues: 16-225, F', 227-259 <MOR>
A;Residues: 16-225, F', 221-232, 1993
Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties of a recombinant zymogen of the A;Reference number: 154409; MUID: 94041399
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    A;Accession: A44622
A;Aoleoule type: mRNA
A;Residues: 467-546;550-595;752-764 <WOO>
A;Cross-references: GB:J00185; GB:J00186
A;Oross-references: GB:J00185; GB:J00186
A;Nole. J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
J. Biol. Chem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human complement factor B.
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A; Molecule type: protein
A; Rolecule type: protein
A; Residues: 270-329 < KNIE>
A; Note: binding site for carbohydrate to lysine under artificial conditions
B; Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
A; Titler: Internal homologies of the Ba fragment from human complement component factor
A; Reference number: A44628; MUID:84158524
A; Accession: A44628
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A; Molecule type: protein; mRNA
A; Molecule type: protein; mRNA
A; Residues: 26-764 <MOL>
A; Cross-references: GB: K01566
A; Note: nucleic acid translation differs from the sequence shown in having 300-Leu, 32
A; Note: 736-Ser was also found
A; Note: 736-Ser was also found
A; Note: 736-Ser was also found
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A; Note: 736
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A;Residues: 339-509 <CA1>
A;Cross-references: GB;J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Cross-references: GB;J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Cross-reference GB;J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Title: Cell-specific expression of the human complement protein factor A;Reference number: A25971; MUID:87102880
A;Reference B25911
A;Residues: 1999 <WULP.
A;Residues: 1-99 <WULP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Molecule type: protein
A.Residues: 260-256, T', 298-764 <CHR>
R.Campbell, R.D.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene coding
A;Reference number: A19947; MUID:83273641
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A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 346-764 <CAM>
A;Cross-references: GB:J00125
A;Accession: B19947
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Search completed: August
Job time: 254 sec
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A; TITLE: Cloning of human type VII collagen. Complete primary sequence of the alphal(VII A; Reference number: A54849; MUID:94327588
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A; Residues: 815-892, 'E', 894-1439 <PAR>
A; Residues: 815-892, 'E', 894-1439 <PAR>
A; Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A; Experimental source: Keratinocyte
A; Edammon, W. R.; Abernethy, M. L.; Padilla, K. M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
A; Reference number: 156328; MUID:93107742
A; Status: translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mSS1236; MID:3262308; PIDN:AAB24637.1; PID:9262309
R;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
A; Blol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A;Reference number: A30296; MUID:89139437
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A,Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
A,Note: there are 118 introns
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A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C',
A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C',
A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C',
A; Cross-references: DBBJ-10113694; NID: 9453699; PIDN: BAA02853.1; PID: 9453699
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
Proc. Natl. Acad. Sci. U.S. A. 88, 6931-6935, 1991
A; Title: Human type VII collagen: CDNA cloning and chromosomal mapping of the gene.
A; Reference number: S16316; MUID: 91334380
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A;Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous A;Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous A;Reference number: 148103; MUID:93271985
A;Accession: 184686
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2395-2871, S',2873-2944 <RE2>
A;Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
B;Christiano, A.M.; Ryymaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 11994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser subs
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A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Reference number: A55285, MUD:94224777
A)Contents: annotation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit C;Genetics:
                                                                                                                                                                                                                                                                                                          A; Residues: 1-2944 cCHR>
A; Cross-references: GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125
A; Cross-references: GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125
B; Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A; Title: Molecular cloning and characterization of type VII collagen cDNA.
A; Reference number: PHO844; MUID:92231902
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C;Complex: type VII collagen is probably a homotrimer
C;Function:
                                                                                                                                                                                                                         Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                         Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A30296
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9, 2002, 10:34:15

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F;37-1253/Domain: amino-terminal nonhelical *status predicted <NC1>
F;36-201/Domain: von Willebrand factor type A repeat homology <WwAl>
F;331-318/Domain: fibronectin type III repeat homology <FN1>
F;327-413/Domain: fibronectin type III repeat homology <FN3>
F;327-413/Domain: fibronectin type III repeat homology <FN3>
F;588-53/Domain: fibronectin type III repeat homology <FN4>
F;588-53/Domain: fibronectin type III repeat homology <FN6>
F;588-77/Domain: fibronectin type III repeat homology <FN8>
F;686-77/Domain: fibronectin type III repeat homology <FN8>
F;686-77/Domain: fibronectin type III repeat homology <FN8>
F;686-71/Domain: fibronectin type III repeat homology <FN8>
F;864-952/Domain: fibronectin type III repeat homology <FN8>
F;864-952/Domain: fibronectin type III repeat homology <FN8>
F;864-1045/Domain: fibronectin type III repeat homology <FN8>
F;1052-1134/Region: cell attachment (R-G-D) motif F;1189-1253/Region: cell attachment (R-G-D) motif F;208-204/Domain: animal Kunitz-type proteinase inhibitor homology <FN8>
F;286-299/Domain: animal kunitz-type proteinase inhibitor homology <FN8>
F;286-294/Domain: animal kunitz-type proteinase inhibitor homology <FN8>
F;286-294/Domain: animal kunitz-type proteinase homology <FN8>
F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD -- SKDHVFPVNDGFQALQGIIH 187
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24.1%; Pred. No. 2.9;
ive 42; Mismatches 85;
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Best Local Similarity 24.1%
Matches 52; Conservative
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Human protein sequ
A human TANGO 216
                                                                                                                                   (without alignments)
275.051 Million cell updates/sec
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Human gene 4 encod
Human TANGO 197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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1536
1 GQGGRREDGCPACYGGFDLY......GLSFISSSVIITTHCSDGS 295
                                                                                                             August 9, 2002, 10:32:10 ; Search time 119.13 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAB92985
AAB18456
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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_			770	50.1	487	21	AAB18458		murine TANGO
		13	769	50.1	487	21	AAB18460		
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			166	0	1155	19	AAW72835		Mouse alpha-d #1.
			166		1155	5 6	AAW65102 AAW60002		Mouse beta-integri Mouse albha d bolv
			166	10.8	1155	50	AAW73346		Mouse alphad prote
			166		1161	12	AABU/3/2 AAR78168		Mouse alpha d subu
			166		1161	18	AAW23061		Mouse beta 2 integ
			166		1161	13	AAW72836 AAW65103		Mouse alpha-d #2. Mouse beta-integri
			166		1161	13	AAW60003		Mouse alpha d poly
			166	0.0	1161	20	AAW73347		Mouse alphad prote
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			59.5	0	1151	13	AAW72834		σ.
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	QI	NE01	439 sta	standard;	Protein;		403 AA.		
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	XX XX	Нишап	gene 4	encoded		secreted	a protein HWLFRU2,	SEQ 1D	NO:94.
	ΚW	Human;	; secre	secreted protein;	otein;	pro	proliferative	disorder; cancer;	r; tumour;
	ΚW	foeta	l abnoi	cmality	'; deve	lopm	ental abnor	mality; haemato	poietic disorder;
	X X	inflar	e syste mmatior	em disc	order;	ALUS	; autoimmun logical dis	order: Alzheime:	matold arthritis; r's disease:
	X	Parki	uson's	diseas	ie; cod	niti	ve disorder	; schizophrenia	asthma;
	KW	skin	disorde	er; psc	riasis	se :	psis; dlabe	tes; atheroscle	skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
	X.	cardi	ovascul	lar dis	order;	ang	iogenic dis	order, kidney d	tsorder;
	X X	gastru	ointesi rine di	inai c Sorder	isorde	r; p	gastrointestinai disorder; pregnancy-related endocrine disorder; infection; wound healing	lated disorder; aling; vulnerary	
	ΚM	cell	culture	e; cher	chemotaxis; food	ę.	cell culture; chemotaxis; food additive; gene	gene :	
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	SO	Ношо	sapiens						
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	FT	key Peptide	de	3 -	.27	/vūna	Location/Qualifiers 127		
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WO200134626-A1 17-MAY-2001

Amino acid sequenc A human TANGO 216 A human TANGO 216 Human novel extrac Amino acid sequenc

AAB18455 AAB18457 AAU19662 AAB18448

AAB18447

267 lnekpfsvedtyllcpapilkevgmkaalqvsmndglsfisssviittthcsdgs 321

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AMD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE0145-AAE01513 represent the proteins they encode. CC AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the emount of the new protein in a sample or by determining the presence of mountations in the new genes. Specific uses are described for each of the untations in the new genes. Specific uses are described for each of the proliferative disorders; cancer, tumours foctal and developmental proliferative disorders, diseases of the immune system, allory autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allory autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allory autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allory accorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, schizophrenia, asthma, contintestinal disorders, pregnancy-related disorders, endocrine cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, angiogenic disorders, kidney disorders, continter of primary tissues, to repenerate tissues, to identify their culture of primary tissues, to repenerate tissues, to identify their culture of primary tissues, to repenerate tissues, to identify their conture of primary tissues, to repenerate tissues, to identify their conture of primary tissues, to repenerate tissues, to identify their conture of primary tissues, to repenerate tissues, to identify and alloring partners, and in chemotaxis, and includes specific for a protein of the invention can be used in alleviating symptoms associated with the disorders many or number of immunosorbent assay (ELISA). The present sequence represents a human contribution 
                                                                                                                                                                                                                                       New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRGTTLMKLTEDREQIRQCLEELOKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
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100.0%; Pred. No. 5.3e-157
:ive 0; Mismatches 0;
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                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
01-NOV-2000; 2000WO-US30045.
                                         99US-0163581
2000US-0215133
                                                                                                                                                 Komatsoulis GA,
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                                                05-NOV-1999;
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Gaps

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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                              Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rhemmatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy related disorder; endocrine disorder; mondo healing; vulnerary; endocrine disorder; infection; wound healing; vulnerary; endocrine disorder; chambaxis; food additive; gene therapy;
                                                                                        Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
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                                                                                                                                                                                                                                                                                                                                                                                       "Mature human secreted protein"
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                                                                                                                                                                                                                                                                   binding partner identification; chromosome 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 505-506; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by WGC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Encoded by GKT"
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          AA.
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/note= "Encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Unknown
          AAE01469 standard; Protein; 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2000; 2000WO-US30045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0163581.
2000US-0215133.
                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001.
                                                                       17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                           AAE01469;
                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                        Key
AAE01469
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mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental aborders and include developments for the immune system, aboramalities, haematopoletic disorders, diseases of the immune system, aboramalities, neamatopoletic disorders, diseases, of the immune system, allergies, neurological disorders, (e.g., Alzheimer's disease, strinson's disease), cognitive disorders, schizophrenia, asthma, sylvinson's disease), cognitive disorders, schizophrenia, atheroscierosis, cardiovascular disorders, angiogenic disorders, atheroscierosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked immunosarbent assay (ELISA). The present sequence represents a human cereted protein of the invention.

Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases

(MILL-) MILLENNIUM PHARM INC

30-DEC-1998; 23-DEC-1999;

WPI; 2000-465743/40.

Holtzman DA;

N-PSDB; AAA47455.

99WO-US31025. 98US-0223546.

WO200039284-A1.

06-JUL-2000.

Claim 8; Fig 4; 209pp; English.

Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postiasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chisease, osteoarthritis, Lyme's disease, cachesia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a contraint TANGO expression. A wide range

of cellular disorders can be treated

producing

403 AA; Sequence

ö 181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240 61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120 121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180 Gaps 241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDGS 295 ; Length 403; Indels Score 1524; DB 22; Pred. No. 1.1e-155; 0; Mismatches 2; 99.2%; Query Match Best Local Similarity 99.3 Matches 293; Conservative 87 147 g g ð g à ò ò g ö q

AAB01422 standard; Protein; 333 AA AAB01422 RESULT

(first entry) 20-OCT-2000 AAB01422;

Human TANGO 197.

TANGO: 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatorid arthritis; psortasis; inflammatory bowel disease; septic shock; ulcerative collitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cacherais, autolmmune disease; myasthemia gravis; autolmmune disease; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; human.

Homo sapiens

ö 146 121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180 181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120 Gaps 1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60 ö 241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCS 292 Length 333; Indels 99.0%; Score 1520; DB 21; 100.0%; Pred. No. 2.1e-155; ive 0; Mismatches 0; .; ; Best Local Similarity 100. Matches 292; Conservative 333 AA; Sequence Query Match 147 ò g Ω ò g ò q δ q ò

AAM38976 standard; Protein; 297 AA RESULT AAM38976

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22-OCT-2001 (first entry) AAM38976;

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WPI; 2001-442253/47.
N-PSDB; AAI58132.
                                                                           (HYSE-) HYSEO INC.
                                 WO200153312-A1.
                                                  21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                            Homo sapiens.
                                                             03-AUG-2000;
                                                                14-SEP-2000;
                                                                      29-NOV-2000;
                                                           19-JUL-2000;
                                       26-JUL-2001
                      leukaemia.
                                                                                 Tang YT,
                                                                                    Wang
                                                                                       Zhao
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ъ, В,

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ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                        241 LNE 243
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                                                                                                                                                                                                                                                                                                                                         Human;
                                       147
            121
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AAB92985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful impene therapy: A composition containing a polypucleotide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Include the Activity thes such as: Immune system suppression, Activin/inhibin activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; ONS; Alzhaimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroslis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Yang Y,
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le-127;
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Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO 2121; 10078pp; English.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.2%; Score 1263;
99.2%; Pred. No. le
                                 Human polypeptide SEQ ID NO 2121.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                       2000us-0552317.
2000us-0598042.
2000us-0620312.
2000us-0653450.
2000us-0693036.
2000us-0693036.
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                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263
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specification.

Sequence

Query Match Best Local Simi Matches 241;

61

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The present invention describes primer sets for synthesising 5602

Cull-length cDNAs defined in the specification. Where a primer set

cull-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of

to the complementary strand of a polynucleotide which comprises one of

cligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which complementary to a

sequence and an oligonucleotide comprising a sequence complementary to a

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide sequence complementary to a

complementary strand of a polynucleotide sequence which comprises a 3'-end sequence/3'-end sequence is selected from those defined in

the 5'-end sequence/3'-end sequence is selected from those defined in

the specification. The primers are useful for synthesising polynucleotides,

con a sequence and an olignosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

consistent and/or diagnosis of the abnormality of the proteins encoded by

consistent and specialised methods. AANB3646 to

AANB95893 represent human cDNA sequences; and AANB3622 to AANB362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                        primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto J;
                                                                                                                  181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito K,
Otsuki
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:11706.
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999; 99JP-0248036.
27-AuG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116126
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                     TANGO 266; TANGO 216;; TANGO 261; TANGO 267; TANGO 267; Callular deferentiation; cellular adhesion; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disosas; atelectasis; pulmonary congestion; coedema; emphysema; chronic bronchita; bronchial asthma; bronchied asthma; bronchied stopical asthma; bronchied associated disease; renal disorder; spleën associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; Parian henriation; latrogenic disease; inflammation; meningitis; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO
                                                                                                                                                    RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 173
                                                                                                                                                                PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 233
                                                                                                                                                                                                          MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 113
                                                                                      Gaps
                                                                                                                      Novel human and murine secreted proteins designated TANGO 216, 261, 265, 266 and 267 useful as modulating agents of cellular processes,
                                                                                      ö
                                                              Length 218;
                                                                                     0; Indels
                                                               Score 966; DB 22;
Pred. No. 7.9e-96;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser
                                                                                                                                                                                                                                                                                                                                                                                   A human TANGO 216 polypeptide clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                     AAB18456 standard; Protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
                                                               62.9%;
98.9%;
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            of the present invention.
                                                                                    Matches 188; Conservative
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                                                                                                                                                                                                                                                       234 KINDSVTLNE 243
                                                              Ouery Match
Best Local Similarity
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                                Sequence
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polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Wilebrand factor-associated disorder, requilate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectrasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral cochems, hydrocephalus and encephalitis, and treat hepatic disorders.

Corpeted using information provided.
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gpggllraqeqpscrrafdlyfvldksgsvannwieiynfvqqlaerfvspemrlsfivf 85

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(MILL-) MILLENNIUM PHARM INC.
                                                                01-MAR-2000; 2000WO-US05226.
                                                                                                      e.g. for treating cancer
                                                                                        WPI; 2000-579269/54.
                                                                                           N-PSDB; AAA75149.
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                                                     WO200052022-A1.
                                                                      01-MAR-1999;
                                                           08-SEP-2000
                                                                                  Barnes TM,
                                                                                                                                                                                      Sequence
     Peptide
                 Protein
           Domain
                       Domain
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WPI; 2000-579269/54.
N-PSDB; AAA75157.
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AAB18455
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           Qγ
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                                                                                                                                                                                                            "von Willebrand factor A domain"
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te= "transnmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "extracellular domain"
                                                                                                       "extracellular domain"
                                                                                                                                                                                                                                                                 "transmembrane domain"
                                                                                                                                                                                                                                                                                                                 /note= "cytoplasmic domain"
                                                                                                                                                            "mature protein"
                                                     'note= "signal peptide"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 1A-C; 175pp; English.
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Best Local Similarity 53.2%
Matches 157; Conservative
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describes TANGO 266, TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cell trafficking and/or migration, modulate cellular adhesion, modulate cell adhesion in proliferation disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; schemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; hazheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
180 QALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSV 239
                                                                                                                                                                        120 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGF 179
                                                                                               Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                         240 ILNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDG 294
                                                                                                                                                                                                                                            Fraser CC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                             AAB18455 standard; Protein; 488 AA.
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1 GQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVF 59

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(MILL-) MILLENNIUM PHARM INC.

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cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; latrogenic disease; indfammation; meningitis;
Alzhehmer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, toxoplasmosis, brainmeningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSV
and hematopoietic associated diseases and disorders, atelectasis,
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ARBIBASS-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, and TANGO 267. The TANGO 262 and TANGO 267. The TANGO 262 and TANGO 267. The TANGO 262 callular proliferation, modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, requiate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, adioacters, such as cancer, modulate the proliferation, differentiation and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, reat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart diseases, modulate the proliferation, differentiation, as ischemic heart diseases with the ovaries, and cerebral oedema, cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral codema, corplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Contectial and viral meningitis, and treat hepatic disorders.

Contectial and viral meningitis, and treat hepatic disorders.

Contectial and viral meningitis, and treat hepatic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GOGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVF 59
                                                                                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 TLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDG 294
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                                                      Fraser CC;
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                                                        Sharp JD,
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                                                                                                                                                                                                                                     Disclosure; Page -; 175pp; English.
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                                                        Holtzman DA,
                                                                                                                                                                                                 e.g. for treating cancer
                                                                                              2000-579269/54
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                                                        Barnes TM,
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12-SEP-2000; 2000US-0231988.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233063.
15-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234997.
26-SEP-2000; 2000US-0234997.
29-SEP-2000; 2000US-0234997.
29-CCT-2000; 2000US-0234999.
29-CCT-2000; 2000US-0234999.
20-CCT-2000; 2000US-0244977.
20-CCT-2000; 2000US-0244777.
20-CCT-2000; 2000US-0246787.
20-NOV-2000; 2000US-0246528.
20-NOV-2000; 2000US-0246528.
20-NOV-2000; 2000US-0246528.
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17-NOV-2000;
17-NOV-2000;
          Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial, ophthalmic; cytostatic; antianzbehmers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency vivus; rheumatoid arthritis; multiple sclerosis; accers; hyperproliferative disorder; breast neoplasm; melanoma; sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                                                    Human novel extracellular matrix protein, Seg ID No 312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-018914.
17-MAR-2000; 2000US-018913.
19-MAY-2000; 2000US-019076.
19-MAY-2000; 2000US-0209467.
26-JUN-2000; 2000US-0209467.
26-JUN-2000; 2000US-0216486.
30-JUN-2000; 2000US-0216486.
30-JUN-2000; 2000US-021487.
11-JUL-2000; 2000US-0217487.
14-AUG-2000; 2000US-0224518.
14-AUG-2000; 2000US-0224518.
14-AUG-2000; 2000US-0225214.
14-AUG-2000; 2000US-0225214.
14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225267.
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2000US-0226868
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                      06-DEC-2001 (first entry)
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14-AUG-2000; 2
14-AUG-2000; 2
18-AUG-2000; 2
22-AUG-2000; 2
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23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
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420 ttsvkpvsvqlnsmlcpapilnkagetldvsvsfnggksvisgslivtaxxcsng 474
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                                                                                           AAB18448;
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                                                   AAB18448
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                                                                                           The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPS). The novel human secreted extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPS may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPS. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPS in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV) (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperpoliferative discorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and carrived as a disease), neurological diseases (e.g. Alzheimer's disease, server a product of a product of a cardiac and antiple of cardial and antiple of cardial diseases (e.g. Alzheimer's disease).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVI 119
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                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, eAlzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 TLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 294
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Pred. No. 8.5e-75;
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                                                                                                                                                                                                                Ruben SM;
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                                                  2000US-0256719.
2000US-0251479.
2000US-0251856.
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            2000US-0250391
2000US-0251030
                                     2000US-0251988
                                                                                         2000US-0251868
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Best Local Similarity
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08-DEC-2000;
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08-DEC-2000;
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hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain hernlation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                                                                                                                                                               cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer;
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                                                                                                                                                                                                                                                                                             TANGO 216;; TANGO 261; TANGO 262; TANGO 267
                                                                                                                                                                                                                           Amino acid sequence of a murine TANGO 216 polypeptide.
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te= "transnmembrane domain"
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AAB18448 standard; Protein; 487
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                                                                                                                                                  (first entry)
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N-PSDB; AAA75150.
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(MILL-) MILLENNIUM PHARM INC.

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           disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the disease, cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
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Best Local Similarity 52.8%
Matches 150; Conservative
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC cellular differentiation and/or modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, condulate cell adhesion in proliferative disorders, such as cancer, and cell trafficking and/or migration, and/or function of cells cand hematopoietic associated diseases and disorders, atelectasis, bronchial pulmonary congestion or oedema, emphysema, chronic bronchial, bronchial conducter renal disorders, spleen associated astemates, modulate the proliferation disorders, spleen associated as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, cartilage associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, treat disorders associated with the ovaries, and cerebral codema, hydrocephalus and encephalitis, alzheimer's bisease, inflammations, brain cancers, bydrocephalus and encephalitis, and treat hepatic disorders.

Contellage associated disease, multiple sclerosis, brain cancers, bydrocephalus and encephalitis, and treat hepatic disorders. It was notes the present sequence does not appear in the specification; it was notes.
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52.8%; Pred. No. 4.1e-74;
iive 52; Mismatches 80;
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                           Sharp JD,
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Best Local Similarity 52.8
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cescribes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular adhesion. modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, differentiation, and/or function of cells modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, bulmonary congestion or cedema, emphysema, chronic bronchitis, bronchial sthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral codema.

CC cartilage associated with the ovaries, and cerebral codema, bacterial and viral meniations, disease, inflammations, brain herniations, disease, cerebral toxpelasmosts, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disease, in the specification; it was note: the present sequence does not appear in the specification; it was created using information provided.
                                                                                               TANGO 266; TANGO 216;; TANGO 261; TANGO 267; TANGO 267; CACILULAR PROFILE TANGO 267; TANGO 267; TANGO 267; TANGO 267; TANGO 2611, TANGO 267; CACILULAR DEFEATION; CELLULAR GIFFERATION; CELLULAR GIFFERATION; CACILULAR GIFFERATION; CACILULAR GIFFERATION; CACILULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION CONGRETION; CACICULAR GIFFERATION CACICULAR GIFFERATION CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFFERATION; CACICULAR GIFF
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                                  A murine TANGO 216 polypeptide clone
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Query Match 50.1%; Score 769; DB 21; Length 487; Best Local Similarity 52.8%; Pred. No. 5.3e-74; Matches 150; Conservative 52; Mismatches 80; Indels 2; Gaps 1;

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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated adsorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchietasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; hydrocephalus; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                               191 KKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVED
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                                                                                                                                                         131 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
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275 ssilcpapvlnkdgetlevsisyndgksavsrsltitatectng 318
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asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the prollication, differentiation, and/or for function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral menigitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple scalerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
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Matches 149;
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                                             Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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                                                                                                                                       Claim 8; Fig 27; 209pp; English.
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Best Local Similarity 99.3%;
Matches 134; Conservative
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Job time: 130 sec
           WPI; 2000-465743/40.
N-PSDB; AAA47479.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:30:02; Search time 98.32 Seconds (without alignments) 655.123 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-970-076-2 1914 1 MATAERRALGIGFOWLSLAT......VIIKEVPPPPAEESEENKIK 368

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

528882 segs, 175299045 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Sequence 12380, A Sequence 1, Appl1 Sequence 257, App Sequence 61, Appl Sequence 61, Appl Sequence 63, Appl Sequence 7, Appl Sequence 2, Appl Sequence 3, Appl Sequence 59, Appl Sequence 1591, App Sequence 1591, App Sequence 27, Appl Sequence 27,	Sequence 34, Appl
US-10-155-881-22380 US-09-805-354-1 US-10-155-881-33525 PCT-US02-19669-61 PCT-US02-19669-61 US-10-177-293-61 US-10-177-293-61 US-01-177-293-63 US-60-360-364-2 US-09-805-354-2 US-09-805-354-3 US-10-150-811-4 US-10-155-881-28757 PCT-US02-19669-27 US-10-157-293-77 US-10-177-293-27	US-09-904-920A-34
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ALIGNMENTS

	Gaps	N 60	M 120 H M 120	v 180 180	V 240	IN 300 IN 300
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SN	Length 56 Indels	MATAERRALGIGFQWLSLATLVLICAGOGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 	EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELOKVLPGGDTYM 	HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 	KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFOVV 	VRCNGFRHARNVDRVLCSFKINDSVTLNERPFSVEDTYLLCPAPILKEVGMKAALQVSMN
GULT 1 -US02-08253-187 equence 187, Application PC/TUS0208253 equence 187, Application PC/TUS0208253 equence 187, Application PC/TUS0208253 aPPLICANT: St. Croix, Brad APPLICANT: St. Croix, Brad APPLICANT: Vogelstein, Bert APPLICANT: Vogelstein, Bert APPLICANT: Wogelstein, Bert APPLICANT: Wogelstein, Bert APPLICANT: Wogelstein, Bert APPLICANT: Wometh TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS FILE REFRENCE: 1107 00179 CURRENT APPLICATION NUMBER: 60/202,0825 PRIOR APPLICATION NUMBER: 60/202,850 PRIOR APPLICATION NUMBER: 60/308,829 PRIOR FILING DATE: 2001-04-11 PRIOR FILING DATE: 2001-08-01 NUMBER OF SEQ ID NOS: 359 SOFWWARE: FastSEQ for Windows Version 4.0 LENGTH: 564 TYPE: PRT ORGANISM: Homo sapiens	l; Ler 166; 0; Ir	SGFDLYE SGFDLYE	JIROGLE 	SEREANS 	CEILAA! EILAA!	CPAPILI CPAPILI
SSSION	DB 2.1e-	SGPACY(TEDREC	SDLFFY:	TLKKSC - - - 	SDTYLL SDTYLL
153 C EXPRE 2/08255	1894 1. No. Lsmatcl	GRREDO 	STTLMKI STTLMKI	PDGELHI PDGELHI	OGIIHS OGIIHS	SKPFSVI IIIII SKPFSVI
T-USO2-08253-187 T-USO2-08253-187 Sequence 187, Application PC/TUSO208253 GENERAL INFORMATION: APPLICANT: CATSON-WALTER, Eleanor APPLICANT: St. Croix, Brad APPLICANT: Nogelstein, Bert APPLICANT: Kinzler, Kenneth TITLE OF INVENTION: ENDOTHELIAL CELL EXPRE FILE REFRENCE: 1107, 00179 CURRENT APPLICATION NUMBER: 60/282,850 PRIOR APPLICATION NUMBER: 60/282,850 PRIOR APPLICATION NUMBER: 60/308,829 PRIOR APPLICATION NUMBER: 60/308,829 PRIOR FILING DATE: 2001-04-11 PRIOR APPLICATION NUMBER: 60/308,829 PRIOR FILING DATE: 2001-04-11 PRIOR FILING DATE: 2001-08-01 NUMBER OF SEQ ID NOS: 359 CENTWARE: FRASEEQ for Windows Version 4.0 SEQ ID NO 187 LENGTH: 564 TYPE: PRT CREANISM: Homo sapiens TYPE: PRT	; Score 1894; DB 1; Logs, pred. No. 2.1e-166; 0; Mismatches 0;	LICAGO	IVESTRO	SVIIALS	OGFQAL(OGFQAL(SVTLNI
ULT 1 -USO2-08253-187 equence 187, Application PC/TUSO2 equence 187, Application PC/TUSO2 expelicant: Carson-Walter, Eleanor APPLICANT: St. Croix, Brad APPLICANT: Vogelstein, Bert APPLICANT: Winzler, Kenneth TITLE OF INVENTION: ENDOTHELIAL C ELE REFERENCE: 1107.00179 CURRENT FILING DATE: 2002-04-10 PRIOR FILLING DATE: 2001-04-11 PRIOR FILLING DATE: 2001-04-11 PRIOR FILLING DATE: 2001-08-01 NUMBER OF SEQ ID NOS: 359 SOFTWARE: FESTERO FO WINGOWS VER EQ ID NO 187 LENGTH: 564 TYPE: PRT ORGANISM: HOMO Sapiens	* Ö	SLATEVI	LEMSF]	GYRTAS 	IVE PVNI IVE PVNI	SFKIN
ULT 1 -US02-08253-187 equence 187, Application PC/T ENERAL INFOMATION: APPLICANT: Carson-Walter, Ele APPLICANT: St. Croix, Brad APPLICANT: St. Croix, Brad APPLICANT: Vogelstein, Bert APPLICANT: Kinzler, Kenneth TITLE OF INVENTION: ENDOTHELI FILE REFERENCE: 1107,00179 CURRENT APPLICATION NUMBER: 60/PRIOR APPLICATION NUMBER: 60/PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 2001-04-11 PRIOR FILING DATE: 2001-04-11 FILENGTH: 564 TYPE: PRT ORGANISM: HOMO SAPIENS	vat	GFOWLS	IKFISP(KFISP(YYENR	ADSKDE 	WDRVLC WDRVLC
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Gaps
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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 359
SOFTHARE: PSSEC FOR Windows Version 4.0
SEQ ID NO 232
LENGTH: 564
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                                                                                                                                              Sequence 232, Application PC/TUS0208253 GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
PCT-US02-08253-232
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PCT-US02-08253-232
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361 ESEE 364
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301 DGLSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAE 360
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APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 4.65F2
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARR: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
TYDE: NO. 1823
LENGTH: 564
TYDE: NO. 1823
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APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Winzler, Menneth
TITLE OF INVENTION: EMOOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00179
CURRENT APPLICATION NUMBER: PCT/USO2/08253
CURRENT FILING DAFE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PLING DAFE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DAFE: 20001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 194
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100.0%; Pred. No. 2.1e-166;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 364; Conservative
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US-60-389-987-1823
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ESEE 364
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                                                                                                                                                                                                                                                                                                       APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OSKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-233-999
CURRENT APPLICATION UNBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
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GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
                                  ARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS
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Best Local Similarity 100.0%; Pred. No. 6.8e-145;
Matches 320; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                       Sequence 18, Application US/10038307 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-038-307-18
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US-10-038-307-18
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                                                                                                                                                                                                                                                                                        LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                                                                                                                          EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
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                                                                                                                                                      ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
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                                                                                                    Indels
                                                                    Length
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APPLICANT: CALSON-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAT
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/382,850
PRIOR APPLICATION NUMBER: 60/382,850
PRIOR APPLICATION NUMBER: 60/309,829
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 50/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1793; DB 1;
Pred. No. 4.4e-157;
5; Mismatches 8;
                                                                Score 1793; DB 1;
Pred. No. 4.4e-157;
5; Mismatches 8;
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PCT-US02-08253-301
Sequence 301, Application PC/TUS0208253
GENERAL INFORMATION:
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96.1%;
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ilarity 96.1%;
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; ORGANISM: Mus
PCT-US02-08253-194
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Best Local Simi
Matches 342;
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Best Local 8
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                               86.2%; Score 1649; DB 6;
100.0%; Pred. No. 9e-144;
tive 0; Mismatches 0;
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US-10-038-307-26
; Sequence 26, Application US/10038307
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
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Best Local Similarity 100.
Matches 318; Conservative
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US-10-038-307-20
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US-10-038-307-20
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LENGTH: 564
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ORGANISM:
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/10038307

Sequence 24, Application US/10038307

GENERAL INFORMATION:
APPLICANT: Theresa L. O'KEFF
APPLICANT: Theresa L. O'KEFF
APPLICANT: Theresa L. O'KEFF
APPLICANT: Theresa L. O'KEFF
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ 1D NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 4.6e-144;
ive 0; Mismatches 0:
                                                                                                                                                  Score 1649; DB 6; I
Pred. No. 4.4e-144;
                                                                                                                                             FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
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Best Local Similarity 100.
Matches 318; Conservative
                                                                                                                                                         Query Match 86.23
Best Local Similarity 100.0
Matches 318; Conservative
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ORGANISM: Homo sapiens
                                                                                                     ) ORGANISM: Homo sapiens
US-10-038-307-2
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; LENGTH: 345
                                                                                               TYPE: PRT
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAFILKEVGMKAALQVSMN 300
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                  Sequence 20, Application US/10038307
Sequence 20, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Haresa L. O'REFE
APPLICANT: Engin OZKARNAK
TITLE REPERENCE: 7853-253-999
CURRENT FILLIAN UNBER: US/10/038,307
CURRENT FILLS APPLICATION NUBER: 202-06-28
NUMBER OF SEQ ID NOS: 26
SOFWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: DIGIN OZKAYNAK
APPLICANT: DIGIN OZKAYNAK
APPLICANT: JUGIN J. HEALEY
TITLE OF INVENTION: THOSO 197
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 543
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                   SGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 GAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTI
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Pred. No. 6e-142;
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                                                                                                                                                                                                                                                                318
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CORGANISM: Homo sapiens
US-10-038-307-14
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100.0%; Pred. No. 6.8e-143;
ive 0; Mismatches 0;
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Pred. No. 9.9e-143;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
TILLE OF INVENTION: Tango 197 and Tango 216 Conf. FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SED ID NOS: 26
NUMBER OF SED ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Theresa L. O'KEFFE
APPLICANT: ENGIN OZKATVAKA
APPLICANT: JUGITH J. HENEY
TITLE OF INVENTION: Tango 197 and Tango 216 Cor
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
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Best Local Similarity 97.2
Matches 318; Conservative
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                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-26
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US-10-038-307-22
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Best Local Similarity
Matches 316; Conserv
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US-10-038-307-22
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LENGTH: 342
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98.4%; Pred. No. 5.1e-141;
ive 0; Mismatches 3;
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Pred. No. 6e-142;
0; Mismatches 2;
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
TILE OF INVENTY TARGE 19
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                   APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/20/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARRE: FASLSEQ for Windows Version 4.0
SSOFTWARRE: FASLSEQ for Windows Version 4.0
US-10-038-307-16; Sequence 16, Application US/10038307; GENERAL INFORMATION:
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98.8%;
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CORGANISM: Homo sapiens
US-10-038-307-10
                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-038-307-16
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Best Local Similarity
Matches 316; Conserv
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Best Local Simi.
Matches 317; (
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EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
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              Sequence 12, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'REFF
APPLICANT: Horizon L. O'REFF
APPLICANT: Trango 197 and Tango 216 Compositions and Methods
TITLE REPRENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
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MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
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Pred. No. 6.3e-129;
3; Mismatches 10;
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                                                                                                                                                                                                                                                                                                           301 DGLSFISSSVIITTHCSDGS 321
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93.98;
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CRCANISM: Homo sapiens
US-10-038-307-12
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US-10-038-307-12
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Best Local Si
Matches 294;
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Gaps

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Indels

Conservative

Db 298 SVIITTTHSSPKS 310

Search completed: August 9, 2002, 10:35:55 Job time: 353 sec

(OT98U) NNAJE BLANK (USPTO)

Run

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Sequence 43, Appl
Sequence 43, Appl
Patent No. 5424399
Sequence 3, Appli
Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, W. Mich APPLICANT: Gallatin, W. Mich APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit CORRESPONDENCES: 51
                        Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.7%; Score 166; DB 1; Lv
28.2%; Pred. No. 4.2e-09;
Live 42; Mismatches 96;
US-08-605-672-2
US-08-605-672-55
US-08-605-672-99
US-08-482-293A-29
US-08-482-293A-99
US-08-943-363-99
US-08-943-363-99
US-09-193-043-2
US-09-193-043-5
US-09-193-043-5
US-09-193-043-99
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5424399-2
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US-08-286-889-3
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTONREY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
PELECOMMUNICATION INFORMATION
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1155 amino acids
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Best Local Similarity 28.2°
Matches 66; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATTERISTICS:
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Sequence 46,
Sequence 43,
Sequence 53,
Sequence 53,
Sequence 53,
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Sequence 46,
                                                                                                                                                   Search time 45.48 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/laa/Parus_COMB.pep:*
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                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-48-18-46
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US-08-95-55-55
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                                                                                                                                                 August 9, 2002, 10:30:01;
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                             95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                         204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                              149 IDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                           200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                    | : | | : | | : | | : | | | : | | | 316 KVGN-FVALRSIQRQIQEK---IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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28.2%; Pred. No. 4.2e-09;
ive 42; Mismatches 96; Indels 3
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REGISTRENDE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/173,497
APPLICATION NUMBER: 08/173,497
FILING DATE: 23-DEC-1993
FRICK APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 28.2%
Matches 66; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-362-652-46
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                                                                                                                                                                                                                                                                                                95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                                                                                                204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                    149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
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APPLICANT: Van de
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STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-193
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 46:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.74
Best Local Similarity 28.24
Matches 66; Conservative
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US-08-485-618-46
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204 FTEFKSSLSPQSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
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                                                             259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                               APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                     16 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                         200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFOVVVRGNGFRHARNVD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRICE APPLICATION NUMBER: US 08/286,889
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
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US-08-482-293A-46
; Sequence 46, Application US/08482293A, 2 patent No. 5831029
; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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Best Local Similarity 28.2<sup>3</sup>
Matches 66; Conservative
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COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO:
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                                          149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                     Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
GAPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5817515e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                           200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.7%; Score 166; DB 2; Length 1155; 28.2%; Pred. No. 4.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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CITY: Chicago
STATE: 111,1nois
COUNTRY: United States
7.IP: 60606-6402
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Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-605-672-46
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/08485618
Sequence 10, 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                              DB 4; Length 1155;
4.2e-09;
thes 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.7%; Score 166; DB Best Local Similarity 28.2%; Pred. No. 4.2e-Matches 66; Conservative 42; Mismatches
                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Wonica
TITLE DE INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER PILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1997-10-03
NUMBER: OF SEQ. DI NOS: 114
                                                                                                                                                                                 US-09-193-043-46; Sequence 46, Application US/09193043; Patent No. 6251395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus US-09-193-043-46
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US-08-485-618-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 IDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                          37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
             149 IDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                  200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                           ; Score 166; DB 2; Length 1155;
; Pred. No. 4.2e-09;
42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                        3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: 111hois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                      Sequence 46, Application US/08943363 Patent No. 5837478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.2%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-943-363-46
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144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
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Patent No. 5817515
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GENERAL OF THE OF INVENTION: No. 581751561 Human 2 Integrin Alpha Subunit NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/13,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-40G-1994
ATTORNEY-AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.7%; Score 166; DB 1; Best Local Similarity 28.2%; Pred. No. 4.3e-09; Matches 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                             27866/32391
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 1161 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear; MOLECULE TYPE: protein US-08-362-652-53
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Patent No. 5766850
GENERAL INFORMATION:
GALLAtin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%; Score 166; DB 1; Length 1161;
28.2%; Pred. No. 4.3e-09;
Live 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive, 6300 Sear Tower
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27866/32797
                                                                                                                                                                                           CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
APPLICATION NUMBER: US 08/362,652
RILING DATE: 21-DEC-1994
APPLICATION NUMBER: US 08/362,652
RIGHTONEY AGENT INFORMATION:
NAME: WALLIAMS JT., JOSEPH A.
REGISTARTION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-4,
TELEFAX: 312-4,
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
"VPE: amino acids
"'PE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTR: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.29
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-485-618-53
                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-362-652-53
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FILLING DAIL:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILLING DATE: 23-DEC-1993
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG'1994
PRIOR APPLICATION NUMBER: US 08/36,652
FILING DATE: 21-DEC-1994
APTICATION NUMBER: 38,659
FILING DATE: 31-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6348
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TTYPE: amino acids
TTYPE: amino acids
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COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
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APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-482-293A-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53, Application US/08482293A
Sequence 53, Application US/08482293A
Batent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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28.2%; Pred. No. 4.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                      ALIGNAL MARKER MILLIAMS Dr., JOSEPH A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPRAX: 312-474-0448
                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
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COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-605-672-53
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Best Local Similarity
Matches 66; Conserv
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STREET: ...
TTY: Chicago
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US-08-482-293A-53
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149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
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                                                                                                                                                                                                                                                       204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                 37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/08943363
Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS: 114
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                           200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.7%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 4.3e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                                                                                                                                         149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                   37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEOGENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | ||: | | : | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
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                                                                                          Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: 111inois COUNTRY: United States
                                                                                                                                                96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.3%; Score 159.5; DB 1; Best Local Similarity 27.9%; Pred. No. 2.2e-08; Matches 63; Conservative 41; Mismatches 93;
                                                                                             Query Match 8.7%; Score 166; DB 4; Best Local Similarity 28.2%; Pred. No. 4.3e-09; Matches 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27
PELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFRAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IELEKA: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RY: United States
60606-6402
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; ORGANISM: Mus musculus US-09-193-043-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | || : | | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 166; DB 2; Length 1161;
; Pred. No. 4.3e-09;
42; Mismatches 96; Indels 3
                                                                                                   FILING DATE: 43-00-100

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38.659
REFERENCE/DOCKET NUMBER: 27866/32684
TELEPHONE: 312-474-6300
TELEPAX: 312-474-6300
TELEFAX: 312-474-0448
: TELEFAX: 312-474-0448
: TELEFAX: 312-474-0468
: INFORMATION FOR SO ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/09193043
Patent No. 6251395
GENERALINFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE COF INVENTION: No. 6251395e1 Human 2
FILE REPERENCE: 27866/35004
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: US/09/193,043
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
                  CLASSIFICATION: 530
PRIOR APPLICATION DAPR:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.7%;
Best Local Similarity 28.2%;
Matches 66; Conservative 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-943-363-53
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                                                                                                                                                                                                                            157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 207
                                                                                                                                                                                                                                                                                                                                                                                       DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37, Application US/08485618
Sequence 37, Application US/08485618
Sequence 37, Application US/08485618
Sequence 37, Machael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STARE: 1111nois STARE: 1111nois COUNTRY: United States 2IP: 6060-6402 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: DAY SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHIL Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: DATA: D
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8.3%; Score 159.5; DB 1;
Best Local Similarity 27.9%; Pred. No. 2.2e-08;
Matches 63; Conservative 41; Mismatches 93;
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REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
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44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE---- 97
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Job time: 182 sec
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0992z1 mus musculu
09xtp6 plasmodlum
09ff49 arabidopsis
097566 canis famil
099564 mus musculu
091900 xenopus lae
001510 plasmodlum
0923x3 mus musculu
09644z strongyloce
018048 caenorhabdi
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096c67 homo sapien
09gzfs caenorhabdi
001506 plasmodium
001508 plasmodium
                                    Q21281 caenorhabdi
Q964n4 caenorhabdi
O00261 homo sapien
Q966ft5 homo sapien
9p218 homo sapien
9bqu7 homo sapien
Q63870 mus musculu
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Q63001 rattus norv
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Q94674 plasmodium
Q948g7 oryza sativ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; "Identification of the Cellular Receptor for Anthrax Toxin.";
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Last sequence update)
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 Nature 414:0-0(2001)
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096cc6 homo sapien
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099ye7 rattus norv
09bpg8 halocynthia
004588 eimeria max
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090819 neospora ca
043853 homo sapien
090903 homo sapien
028984 sus scrofa
091330 rattus norv
091330 rattus norv
096877 mus musculu
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                       Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Ninomiya K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Kawai Hio Y., Sato K., Wishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Sekine M., Kikuchi H., Murakawa K., Sato K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Subohuman cDNA sequencing project.";
Submitted (Cor-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO55636; BAB709761; --
SEQUENCE 245 AA, 26111 MW, BIAEGEBOAZEBEEOG CRC64;
                                                                               241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TYTVNETYTTSVKPVSVQLNSMLCPAPILNKAG------EWGLTVTQAGVKWHDLTH
                                   241 VRGNGFRHARNYDRVLCSFKINDSVTLNERPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.0%; Score 574; DB 4; Length 245; ilarity 49.2%; Pred. No. 2.2e-42; Conservative 45; Mismatches 67; Indels
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Last annotation update)
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01-DEC-2001 (TREMBLrel. 19, Last seque
01-DEC-2001 (TREMBLrel. 19, Last annot
CDNA FL331074 FIS, CLONE HSYRA2001476.
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Matches 120; Conserv
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361 ESEENKIK 368
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Q96EC6;
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Q96NC7;
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Q96EC6
ID Q90
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Q96NC7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 FQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKÄÄLQ 296
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                 Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 97;
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003908; AAH03908.1; -- Hypothetical protein.
NON_IER
                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC012475; AAH12475.1; -. NON.TER 1 SEQUENCE 97 AA; 10453 MW; 14F475F0B170E71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31AB702E42E9CEB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 ILFLLLALALLWWFWPLCCTVIIKEVPPPPA---EESEENKI 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %) July-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 19, Last annotation update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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49.0%; Pred. No. 3.4e-17;
cive 21; Mismatches 28; 1
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                         Score 391.5; DB 4;
Pred. No. 6.6e-27;
1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 AA.
                                                                                                                                                                                                                              TISSUE-BREAST, AND MAMMARY ADENOCARCINOMA; Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL 24.5 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 VSMNDGLSFISSSVIITTTHCSDGSILAIA 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 AA; 24505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%;
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Best Local Similarity 49.0%
Matches 50; Conservative
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Matches 81; Conservative
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                        NCBI_TaxID=9606;
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Gaps

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SEQUENCE FROM N.A.
MEDLINE=93149203; PubMed=8426611;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella microneme protein Epi00.";
Mol. Biochem. Parasitol. 57:171-174(1993).
EMBL; M99058; AAA29076_1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 VESTRGTTLMKLTEDREQIRQGLEELQKVLPG-------GDTYMHEGFERAS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 GGRREDGG-----PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
Eimeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 DRI---QLOGYTTYTGRALQKVIRDFDDAYIGNKQVLLLLTDGQAKDNKLILP--NANRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 RDLGAIVYCVGVKDFNETQLARIA---DSKDHVFPVNDGFQALQGIIHSILKKSCIEILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75;
                                                                                                                                                                                                                                                                                                                                                                                        Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Indels
                                                                                                                                                                                                                                                                                                 INTEGRIN ALPHA HR1.
W; 0D9108D2B05CFFAE CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR ANTIGEN HOMOLOGOUS SEQUENCE (EMP100).
                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.0%; Score 153.5; DB 5
Best Local Similarity 24.1%; Pred. No. 0.00019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                 HSSP; P11215; 1A8X.

HSSP; P11215; 1A8X.

InterPro; IPR000413; Integrin_alpha.

InterPro; IPR00303; vWFA.

Pfam; PF00357; integrin_A; 1.

Pfam; PF00352; vwa: 1.

PRINTS; PR00185; INTEGRINA.

SMART; SM00191; Int_alpha; 5.

SMART; SM00191; Int_alpha; 5.
                                                                                                                                                                                                                                                                                                      31 1332 INT
1332 AA; 145852 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000884; TSP1.
InterPro; IPR002035; vWFA.
Ffam; PF00090; tsp_1; 6.
PRINTS; PR00453; VWFADDWAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00209; TSP1; 6.
FMSITE; PS50092; TSP1; 5.
PROSITE; PS50034; VWFA; 1.
SEQUENCE 724 AA; 75808 MW;
  AB048261; BAB21479.1;
                                                                                                                                                                                                                                     PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Conservative
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                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Q04588;
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Q04588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 207
                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE---- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21103187; PubMed=11160215;
Miyazawa S., Azumi K., Nomaka M.;
Cloning and characterization of integrin alpha subunits from the solitary ascidian, Halocynthia roretzi.";
J. Immunol. 166:1710-1715(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%; Score 159.5; DB 11; Length 1161; 27.9%; Pred. No. 4.8e-05; Live 41; Mismatches 93; Indels 29;
                                                                                                                                                                                                                 9
                                                                                                                                                                                                          SEQUENCE 1161 AA; 126600 MW; 2258491A984A705E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 LOGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halocynthia roretzi (Sea squirt).
Eukaryota: Metazoa: Chordata: Urochordata: Ascidiacea:
Stolidobranchia: Pyuridae: Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF01839; FG-GAP; S.
Pfam: PF00357; integrin_A; 1.
Pfam: PF00092; vwa; 1.
PRINTS: PF00185; inTEGRINA.
PRINTS: PR00189; inTEGRINA.
SMART: SM00191; int_alpha; 4.
SMART: SM00327; vwa; 1.
PROSITE; PS50234; vwe; 1.
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                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                      01-DEC-2001 (TrEM)
ALPHA D INTEGRIN.
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=10116;
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Length 712;

DB 5;

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Query Match 7.2%
Best Local Similarity 24.7%
Matches 67; Conservative
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                                                                                                                                                                          ---ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP--VNDGFQALQGIIHSI 215
                                                                                                                                                                                                                                                     169 LSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPRYLQSNWGGVSSQINGI 228
                                                                                                                            55 V-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQK 111
                                                                                                                                          58 IGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDLSDSRAQNADLLAAAAK 117
                                                      43; Gaps
                                                                            1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGGPACYGGFDLYFILDKSGS 54
                                                                                             Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
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M Kalleher M., Tomley F.M.;

M "Translant expression of beta-galactosidase in differentiating prorozoltes of Eineria tenella.";

MOL. Biochem. Parasitol. 97:21-31(1998).

R EMBL; AF032905; AAD03350.1; --.

R HSSP, P17301; 1AAOX.

R InterPro: IPR000804; TSP1.

R InterPro: IPR000905; VWFA.

R Pfam; PF000090; tsp_1; 6.

R Pfam; PF000090; tsp_1; 6.

R PRIMTS; SM00209; TSP1; 6.

R SMART; SM00209; TSP1; 6.

R RRANT; SM00209; TSP1; 6.

R PROSITE; PS50031; VWA; 1.
                             Length 724;
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MICRONEME PROTEIN ETMIC-1.
15B8F3C190B70F73 CRC64;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TremBirel. 06, Last sequence update) 01-DEC-2001 (TremBirel. 19, Last annotation update) MICRONEME PROTEIN ETMIC-1 PRECURSOR.
                               DB 5;
                                                       45; Mismatches 109;
                              Score 150.5; DB 5
Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                      712 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Biochem. Parasitol. 49:277-288(1991).
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                                                                                                                                                                                                                                                                                 216 LKKSCIEI----LAAEPSTI--CAGE 235
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=HOUGHTON;
MEDLINE=92131064; PubMed=1775171;
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712 MI
74777 MW;
                              7.9%;
                                                          Conservative
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712 AA;
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                                              Similarity
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                                Query Match
Best Local Simi
Matches 69;
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SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDREQIRQGLEE 108
                                                                                                                                                                                                                                                                                                                                                                                                                               Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; "Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK 51
                                                                                                                                                                        Gaps
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
INTERIN FAMILY.
EMBL; AF109906; AAC84162.1; -.
EMBL; AF409850; AAC85284.1; -.
EMBL; BC011086; AAH11086.1; -.
HSSP; P00761; IEPF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas G., Hood L.;
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01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S).
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                                                                    Indels
; Score 137.5; DB 5;
; Pred. No. 0.0021;
43; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 ALQGIIHSILKKSCIEILAAEPSTI--CAGE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 QVNGIIKAACKDLAKDAVCSEWSEYGPCVGE 254
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001456; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR0020355; WKFA.
Pfam; PF00089; trypsin; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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TISSUE=BREAST TUMOR;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 KEIRHTILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-------NRQGYRTAS- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| | :: :|: | :: | |: ERSQ-----DVTEVIFILEVISAMQSQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV------KD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 GNMSANASDQERTPWQVTFKPKSKETCQGS--LISDQWVLTAAHCFHDIQMEDHHLWRVN 530
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLRMS--FIVFSTRGTTLMKLTE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-20183852; Pubmed-10717300;
Lovett J.L., Howe D.K., Sibley L.D.;
"Molecular characterization of a thrombospondin-related anonymous
                                                                                                                                                                                                                                                          Best Local Similarity 23.5%; Score 134; DB 11; Length 760;
Matches 75; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            765 AA; 82880 MW; 9727838CC1FE8CD4 CRC64;
                                                                                                                                                                                                             91C896A3EDC7D448 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THROMBOSONDIN RELATED ADHESIVE PROFEIN HOWOLOG.
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Mol. Blochem. Parasitol. 107:33-43(2000).
EMBL; AF061273; ARF01565.1; -.
InterPro; IPR001969; ASP_Protease.
InterPro; IPR00884; TSP1.
SMART; SM00327; VWA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 2.
PROSITE; PS00134; TRYPSIN_HIS; UNRNOWN_1.
PROSITE; PS00134; TRYPSIN_SER; UNRNOWN_1.
PROSITE; PS50234; VWFA; 2.
Hydrolase; Serine protease.
SEQUENCE 760 AA; 84741 MW; 91C896A3EI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MND-----GLSFISSSVII 312
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Pfam; PF00092; vva; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                             186 AMTDGESDSD--FHTVNEAKVIRERGGIITVLSVGMYVNHNECRSMCGCRNDSSPCPLYL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTLMKLTEDREQIRQGLEELQKVLP - GGDTYMHEGFERASEQIYYENRQGYRT - - ASVI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVND 203
                                                                                                                                                                                                                                                                                                                                                                          147 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF-NETQLARIADSKDHVFP----V 201
                                                                                                                                                             72 CTSQLDICFLVDSSGSIGEAHYEE----VKQFLHAFLSKLPIGNDEVNTSLVIFSTTVHP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-98003048; PubMed-9344363; MeSSel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.; Type XII collagen contributes to diversities in human corneal and limbal extracellular matrices."; Invest. Ophthalmol. Vis. Sci. 38:2408-2422(1997). EMBL. 1061919; AACO1506.1; ... Interpro; IPR003961; FN_III. Interpro; IPR003961; FN_III. Interpro; IPR003051; VWFA. PÉam; PF00041; fn3; 3. Péam; PF00092; VWA; 1.
                                                                Gaps
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                                                                                                                             39 CYGGFDLYFILDKSGSVLH-HWNEIYYFVEQLAHKFIS-----PQLRMSFIVFSTRGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                LMKL----TEDREQIRQCLEELQKVLPGGDTYMHEGFERASEQIY-YENRQGYRTASVII
                                                            25;
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Length 765;
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                                                                Indels
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Last sequence update)
Last annotation update)
6.9%; Score 132.5; DB 5; 25.1%; Pred. No. 0.0063; tive 35; Mismatches 89;
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01-JUN-1998 (TrEMBLrel. 06, Ls
01-DDC-2001 (TrEMBLrel. 19, Le
TYPE XII COLLAGEN (FRAGMENT).
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SMART; SM00060; FN3; 3.
SMART; SM00327; VWA; 1.
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                                                                Conservative
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517 AA;
                                   Similarity
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Best Local 3
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RECEPTOR MUA-3 PRECURSOR (K08E5.3 PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 -TASVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FN----ETQLARIA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 DSK--DHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 SKPCGDHVFQVNN-FEAVKTIQNQLQEKT----FALEGTQTGSTSSFECEMSQEGFSAA 225
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                      63; Gaps
                                                                                                                                                                                                                                                                                                                                                                  44 DLYFILDKSGSVLHHWNEIYYFVEOLAHKFISP---QLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                                                                                                                                                                                                                       Length 920;
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                                                                                                                                                                                                                                                                                                                                       Indels
Lee J.-K., Schook L.B., Rutherford M.S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U40072; AAB16869.1; -.
HSSP; P11215; 1A8X.
                                                                                                                                                                                                                                                   102440 MW; E96CC51E350DD5AC CRC64;
                                                                                                                                                                                                                                                                                                      6.8%; Score 130.5; DB 6;
26.4%; Pred. No. 0.012;
ve 41; Mismatches 72;
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                                                                    InterPro; PLIALI; Integrin_alpha.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; WWFA.
Pfam; PF041893; FG-GAP; 4.
Pfam; PF001925; VM-3: 1.
PRIWES; PR00195; INTEGRINA.
SMART; SM00191; Int_alpha; 4.
SMART; SM00191; Int_alpha; 4.
SMART; SM00191; Int_alpha; 4.
SMART; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
NON_TER 920 920
SEQUENCE 920 AA; 102440 MW; E96CC5
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Science 282:2012-2018(1998).
EMBL; AF13060; AAD29428-1;
EMBL; 230974; CAA63226.2;
EMBL; 230423; CAA63226.2; JOINED.
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MEDLINE=99069613; PubMed=9851916;
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01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 13, La
01-DEC-2001 (TrEMBLrel. 19, La
TRANSMEMBRANE CELL ADHESION RE
(FRAGMENT).
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Best Local Similarity 26.4%
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 HEDLFFYSERBANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE 97
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

MCBI_TaxID=9823;
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 131; DB 4; Length 660; 29.8%; Pred. No. 0.007; ative 38; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                  Smith M.;
Submitthed (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000): CAB65984.1; -.
HSSP; P11215; 1BHQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660
72523 MW; 3E3A10A285ECAA51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ234P15.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT).
COL12A1.
                                                                                                                                            660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                          204 GFQALQGIIHSILKKSCIEI---LAA 226
                                                 303 -FDAFQRISFELTQSICLRIEQELAA 327
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     028984;
01-NOV-1996 (TrEMBLrel. 01, C.
01-FEB-1997 (TrEMBLrel. 02, L.
01-DEC-2001 (TrEMBLrel. 19, L.
CD11B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003961; FN_III.
InterPro; IPR003961; VWFA.
Pfam; PF00041; fn3; 2,
Pfam; PF00042; vwa; 2,
Prinrs; PR00453; vWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM00327; VWA: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 IHSILKKSCIEI---LAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638 SFELTQSICLRIEQELAA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.83
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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NON_TER
SEQUENCE
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Q28984
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Search completed: August 9, 2002, 10:46:19 Job time: 842 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                                                                                                                                                        R PRINTS; PRO0289; DISINTEGRIN.
R PRINTS; PRO0289; DISINTEGRIN.
R PRINTS; PRO0289; DISINTEGRIN.
R PRINTS; PRO0261; LDLRECEPTOR.
R SMART; SMO018; EGF_CA; 1.
SMART; SMO019; EGF_LA; 1.
SMART; SMO019; EGF_LA; 45.
SMART; SMO0192; LDLA; 4.
SMART; SMO0100; SEA; 2.
SMART; SMO0100; SEA; 1.
R SMART; SMO0100; SEA; 1.
R PROSITE; PSO0101 ASX_HYDROXYL; UNKNOWN_32.
R PROSITE; PSO1187; EGF_1; UNKNOWN_1.
R PROSITE; PSO1187; EGF_2; 6.
R PROSITE; PSO108; LDLAA_2; 2.
R PROSITE; PSO004; SEA; 4.
R
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 19, Last annotation update)
INTEGRIN BETA 2 ALPHA SUBUNIT.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DLYFILDKSGSVLHH--WNEIYYFVEQLA 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3767 AA; 417284 MW; 8DA3AE5EA50AEB8E CRC64;
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                  Interpro: IPR00152; Asx_hydroxyl.
Interpro: IPR001562; Disintegrin.
Interpro: IPR001561; BGF-like.
Interpro: IPR001881; EGF-Ga.
Interpro: IPR001082; SEA.
Interpro: IPR001082; SEA.
Interpro: IPR0010035; vWFA.
Pfam: PF00108; EGF: 33.
Pfam: PF001390; SEA: 2.
Pfam: PF001390; SEA: 2.
Pfam: PF00092; vwa: 1.
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SEQUENCE FROM N.A.
Fathallah D.M. Sr., Zerria K. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CYGGF------
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SEQUENCE
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SIGNAL
CHAIN
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----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 DGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKIN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 NIAFLIDGSGSI----NTIDF---QKMKEFVSTVMDQFQKSKTLFS-----LMQYSDEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 DSVTLNEKPFSVEDTYLLCPAPILKEVG----MKAALQVSMNDGLSFISSSVI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 6.4%; Score 123; DB 11; Length 1151; Best Local Similarity 23.9%; Pred. No. 0.075; Matches 70; Conservative 46; Mismatches 105; Indels 72;
"Cloning of the rat CD11b CDNA sequence.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
REMBL, AF76859; AAF81280.1; -.
EMBL, AF76859; AAF81280.1; -.
EMBL, AF76859; AAF81280.1; -.
InterPro: IPR000413; Integrin_alpha.
InterPro: IPR002035; vWFA.
Rem: PF00185; integrin_A; 1.
PRINYS; PR01189; FG-GAP; 5.
RPRINYS; PR01189; Integrin_A; 1.
RRSPR: SM00191; Integrin_A.
RSMART; SM00191; Integrin_A.
RSMART; SM00191; Integrin_A.
RPROSITE; PS00242; INTEGRIN_ALPHA; 1.
RPROSITE; PS50224; VWFA, 1.
RPROSITE; PS50234; VWFA, 1.
SEQUENCE 1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;
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(without alignments) 572.831 Million cell updates/sec
                                                                                                                                                                                                                                  1 MATAERRALGIGFQWLSLAT......VIIKEVPPPAEESEENKIK 368
                                                                                                                  61.73 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                August 9, 2002, 10:30:01; Search time
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                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1914
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                                                                                                                  Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

283138

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_71:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	noradi rassa	antigen Em100 - Ei	cell surface glyco	surface	collagen alpha i(X	leukocyte surface	immunodominant mic	collagen alpha 1(X	classica	collagen alpha 1(X		hypothetical prote	cartilage matrix p	type XII collagen	complement factor	collagen alpha 1(V	complement factor	collagen alpha 2(V	cartilage matrix p	cartilage matrix p	complement factor	hypothetical prote	sporozoite surface	hypothetical prote		•	thrombospondin-rel	dnaK protein (heat	hypothetical prote	kinesin-like prote
SUMMARIES		A48569	RWHU1B	RWHU1C	A40020	S00551	A45638	A45974	C2MS .	S31212	S78476	S42373	A37979	151027	ввни	A54849	BBMS	S21369	56522	33809	51579	T28797	46283	T23087	E70121	S33578	S04531	196958	T46488	50240
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% Query Match		7.9	7.6	7.5	7.5	7.4	•	٠.	٠.	٠.	6.8		6.3			٠			5.7			5.5					5.5			
Score	100	150.5	145.5	143.5	4	141		137	131	130	130	128	120.5	118	113.5	111.5	110.5	109.5	108.5	107.5	107	105.5	100.5	100	99.5	99.2	66	66	66 6	66
Result		н	7	ო	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT

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undulin 1 - human	A40970	7	843	4.9	94	
integrin alpha-1 c	A35854	7	1180	5.0	95.5	
integrin alpha-E c	A53213	~	1179	2.0	95.5	~
inter-alpha-inhibi	JC5953	~	932	5.0	95.5	~
arginyl-tRNA synth	E87665	~	9	5.0	95.5	_
transcription regu	AF1166	~	334	5.0	95.5	_
probable retroelem	F84811	7	689	5.0	96	39
integrin alpha-1 -	A55348	~	272	5.0	96	_
hypothetical prote	T47637	~	929	5.0	96.5	_
collagen alpha 3(V	A37797	, - 1	3137	5.1	26	
integrin alpha-1 c	A45226	~	1151	5.1	97	32
dnak protein NMB05	н81185	0	642	5.1	97.5	
collagen alpha 3(V	CGHU3A	7	3176	5.1	86	<u>_</u>
hypothetical prote	T04822	~	537	5.1	98.5	~
collagen alpha 2(V	CGHU2A	-	1018	5.2	66	_
collagen alpha 2(V	S09646	~	917	5.2	66	_

ALIGNMENTS

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Gintyen Education measures

Gintyen Education in Marking

Cipate: 01-bec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

Cipates: 01-bec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

Ripcession: A86569

Mol. Biochem. Parasitol. 57, 171-174, 1993

Ayitide: Sequence of a major Einmeria maxima antigen homologous to the Einmeria tenella Ayitide: Sequence of a major Einmeria maxima antigen homologous to the Einmeria tenella Ayitide: Sequence of a major Einmeria maxima antigen homologous to the Einmeria tenella Ayitide is preliminary

Ayocession: A48569

Ayocession: A48669

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP--VNDGFQALQGIIHSI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 V-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 VLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSERE--- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 150.5; DB 2; 25.9%; Pred. No. 0.00039; ive 45; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 LKKSCIEI----LAAEPSTI--CAGE 235
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Matches 69;
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Query Match
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Matches
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A; Residues: 9-1153 <HTC>
A; Residues: 9-1153 <HTC>
A; Residues: 9-1153 <HTC>
A; Cross=references: GB:JOH145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross=references: GB:JOH145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; A; Cross=references: GB:JOH145; NID:g189068; PIDN:AA59903.1; PID:g386975
A; Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
A; Timmunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in number: A46526; MUID:93123748
A; Accession: A46526
A; Status: not compared with conceptual translation
A; Status: not compared with conceptual translation
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A; Residues: 917-1042 <AR2>
A; Residues: 917-1042 <AR2>
A; Residues: 917-1042 <AR2>
A; Cross-references: 917-1044
B; Cross-references: 917-1044
A; Tickes: Co. 10.5; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A; Title: CDNA sequence for the alphaM subunit of the human neutrophil adherence receptor A; Reference number: A32218; MUID:89098893
A; Accession: A32218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A; Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A; Note: part of this sequence, including the amino end of the mature protein, was confir
B; Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Mitle: The promoter of the CD11b gene directs myeloid-specific and developmentally reg
A; Reference number: A41600; MUID:92073318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-9 <- SHES.
A; Cross-references: GB: M76724; NID: g180018; PIDN: AAA58410.1; PID: g553215
A; Cross-references: GB: M76724; NID: g180018; Pierce, M W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A; Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi
A; Reference number: A94193; MUID: 88190151
A; Accession: A30892
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A; Residues: 1-499,501-1153 <FLE>
A; Cross-references: GB:S5227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A; Cross-references: GB:S5227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A; Note: the last three bases of intron 13, CAG, are included in some but not all matura
A; Note: sequence extracted from NCBI backbone (NCBIP:121963)
A; Note: sequence extracted from NCBI backbone (NCBIP:121963)
B; Pierce, M. W.; Remold-OʻDonnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A; Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across:
A; Reference number: A90664; MUID:87076671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A. Accession: A31108
A. Accession: A31108
A. Accession: A31108
A. Accession: A31108
A. Accession: A31108
A. Gross references: GB-103925; NID:9187284; PIDN:AAA59544.1; PID:9307148
A. Cross references: GB-103925; NID:9187284; PIDN:AAA59544.1; PID:9307148
A. Cross references: GB-103925; NID:9187284; PIDN:AAA59544.1; PID:9307148
A. Accession: A283-2158, 1988
A. Accession: A28915; MUID:88257215
A. Accession: A28915
cell surface glycoprotein CD11b precursor [validated] - human human surface glycoprotein CD11b precursor [validated] - human high and complement receptor type 3 alpha chain; leukocyte adhesion protein leukocyte integrin alpha chain; neutrophil adherence receptor alpham chain cyspecias: Homo sapiens (man) cybate: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2000 cybate: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2000 cyaccession: A31108; A28915; A41600; A30892; A3218; A4626; A26091; I52567 cyaccession: A31108; A28915; A4110; Springer, T.A.

J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, 0).
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A; Residues: 17-31 <PIES
A; Experimental source: granulocytes
R; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A31108; MUID:88315033
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RWHUIL

Cell Surface glycoprotein CD11c precursor - human

Cell Surface glycoprotein CD11c precursor - human

N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain

C;Species: Homo sapiens (man)

C;Species: AL: Garcia-Aguilar, J: Springer, T.A.

J: Biol. Chem. 265, 12750-12751, 1990

A;Residues: 1-1163 < COR>

A;Note: this revision to the sequence from reference A35543 includes the carboxyl end

A;Note: this revision to the sequence from reference A35543 includes the Carboxyl end

A;Note: this revision to the sequence from reference A35543 includes the Carboxyl end

A;Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecu

A;Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecu

A;Reference number: A35543; MUD: 90153906

A;Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecu

A;Reference number: DNA

A;Reference number: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene GDB:ITGAM; CR3A
A;Cross-references: GDB:120599; OMIN:120980
A;Gene GDB:ITGAM; L2-16911.2
A;Map position: 16p11.2-16p11.2
A;Note: promoter contains a GATA motif and two Spl consensus binding sites
A;Note: promoter contains a GATA motif and two Spl consensus binding sites
A;Note: promoter contains a GATA motif and spl adhesion; glycoprotein; cell adhesion; glycoprotein; cell adhesion; glycoprotein; heterodimer;
C;Neywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer;
C;Neywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer;
F;17-1108/Domain: signal sequence #status predicted capparatus experimental cMAT>
F;17-1108/Domain: extracellular #status predicted capparatus predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: intracellular #status predicted cTMM>
F;1115-1153/Domain: intracellular #status predicted cTMM>
F;1115-1153/Domain: intracellular #status predicted cINTA>
F;115-1153/Domain: ontains #status predicted cINTA>
F;115-1153/Domain contains #status predicted cINTA>
F;115-1153/Domain contain
                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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A;Residues: 1-834 <CO2>
A;Note: this sequence has been revised in reference A36584
R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
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Blood 79, 865-870, 1992
A;iiie: Characterization of the myeloid-specific CD11b promoter.
A;Reference number: 152567; MUID:92144986
A;Accession: 152567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA
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us-09-970-076-2.rpr

Fri Aug

form

a novel large

end.

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Cigenetics:
A; Introns: 2845/3; 2863/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
A; Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C; Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von C; Keywords: alternative splicing; colled coil; connective tissue; disul F; 1-23/Domain: signal sequence #status predicted csigo
F; 24-3124/Product: collagen alpha 1(XII) chain #status predicted charb; F; 24-3124/Product: collagen alpha 1(XII) chain short splice form #status predict F; 24-314/Domain: IIIA #status predicted ciliA
F; 24-314/Domain: IIIA #status predicted ciliA
F; 33-414/Domain: fibronectin type III repeat homology cFN3A>
F; 33-414/Domain: fibronectin type III repeat homology cN3D>
F; 33-414/Domain: fibronectin type III repeat homology cN3D>
F; 32-301/Domain: fibronectin type III repeat homology cN3D>
F; 31-305/Domain: fibro
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F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F;32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate (Asn) (c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. Molecule type: protein
A. Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
A. Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
B. Dublet, B., 'wan der Rest, 'n'
J. Biol. Chem. 262, 17724-17727, 1987
A, Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of peps
A, Reference number: $22254; MUID:88087065
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDN A;Reference number: A28037; MUID:87317590
A;Accession: A28037
                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: mRNA
A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
A;Cross-references: EMBL:M1/375; NID:q211649; PIDN:AAA48718.1; PID:g211650
A;Note: this sequence has been revised in reference A34485
R;Koch, M; Bernasconi, C.; Chiquet, M.
Bur. J; Biochem. 207, 847-856, 1992
A;Fitle: A major oligomeric fibroblast proteoglycan identified as a novel 1
A;Reference number: S23814; MUID:92362621
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A,Molecule type: protein
A.Residues: 2831-2832, T',2834, R',2836-2843;3002-3014 <DUB>
B,Truueb, J.; Trueb, B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A,Title: The two splice variants of collagen XII share a common 5'
A,Reference number: $28811; MUID:93042014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fil384-1465/Domain: fibronectin type III repeat homology Fil384-1465/Domain: fibronectin type III repeat homology Fil374-1557/Domain: fibronectin type III repeat homology Fil565-1647/Domain: fibronectin type III repeat homology Fil65-1738/Domain: fibronectin type III repeat homology Fil65-1838/Domain: fibronectin type III repeat homology Fil375-1838/Domain: fibronectin type III repeat homology Fil397-2019/Domain: fibronectin type III repeat homology Fil397-2019/Domain: fibronectin type III repeat homology Fil319-2199/Domain: fibronectin type III repeat homology Fil307-2294/Domain: fibronectin type III repeat homology Fil307-2294/Domain: fibronectin type III repeat homology Fil307-2294/Domain: fibronectin type III repeat homology Fil308-2440/Domain: fibronectin type III repeat homology Fi
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non-collagenous NC2 #status predicted <NC2>
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A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S23814
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F;2751-2902/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Goross references: GDB:119758; OMIM:151510
A.Map position: 16p11.2-16p11.2
C.Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home C.Superfamily: cell surface glycoprotein CD11b; won Willebrand factor type A repeat home C.Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1163/Product: cell surface glycoprotein CD1c #status predicted <MAT>
F:20-1163/Domain: extracellular #status predicted <CXT>
F:1108-1133/Domain: transmembrane #status predicted <TMA>
F:1108-1133/Domain: intracellular #status predicted <TMA>
F:1137/Domain: intracellular #status predicted <TMA>
F:1134-1163/Domain: ditracellular #status predicted <TMA>
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obar
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A; Residues: 1-3124 cYAMA
A; Residues: 1-3124 cYAMA
A; Cross-references: GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A; NOTE: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
B; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
A; Biol. Chem. 264, 1977-1977, 8, 1989
A; Title: Type XII collagen. A large multidomain molecule with partial homology to type I
A; Reference number: A34485; MUID:90062079
                                                                                                   A;Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A;Reference number: S00864; MUID:88166645
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                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-755, 'L. 757-1163 <CO3>
A; Residues: 1-755, 'L. 757-1163 <CO3>
A; Residues: 1-755, 'L. 757-1163 <CO3>
A; Residues: 1-755, 'L. 757-1163 <CO3>
A; Note: part of this sequence was confirmed by protein sequencing
C; Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
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A;Residues: 245-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 100
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A; Residues: 2772-2792; 2846-2873 <GOR2>
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Best Local Similarity 24.8%
Matches 55; Conservative
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collagen #status predict

<VWA4>

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A; Note: sequence strated from NCBI Dackbone (NCBIN:77752, NCBIP:77756)
A; Note: sequence extracted from NCBI Dackbone (NCBIN:77752, NCBIP:77756)
A; Note: sequence extracted from NCBI Dackbone (NCBIN:77752, NCBIP:77756)
C; Superfamily: thrombospondin type 1 repeat homology; von Willebrand factor type A repeat homology <WWAl>
F; 48-218-Domain: von Willebrand factor type A repeat homology <WWAl>
F; 309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F; 318-296/Domain: thrombospondin type 1 repeat homology <THR3>
F; 313-493/Domain: thrombospondin type 1 repeat homology <THR4>
F; 494-356/Domain: thrombospondin type 1 repeat homology <THR5>
F; 560-610/Domain: thrombospondin type 1 repeat homology <THR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Eimeria tenella
C;Date: 22-Apr.1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Datession: A45638
R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme protein of A;Reference number: A45638; MuID:92131064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP-----VNDGFQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 PKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLVLVMTDGA- 164
                                                                                                                                                                                            VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
                                                                                                     SGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDREQIRQGLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPLPRRRLA---PCRALSLLVGLLAASFAFSSLQPGATTSSGQDQVCTSLLDVMLVVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 -SNLPSQTRSSAAALRDAGAIVVVLGVGSGVNSSECRSIAGCSTSNCPRYLQSNWSNVTQ
198 IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT
                                                                  DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP
                                                                                                                                                                                                                                                                                                                                 261 INDSVTLNEKPFSVEDTYLLCPAPILKEVG----MKAALQVSMNDGLSFISSS 309
                                                                                                                                                                                                                                                                                                                                                                           immunodominant microneme protein Etp100 - Eimeria tenella
                                                                                                                                                                                                                                             Score 137.5; DB pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 ALQGIIHSILKKSCIEILAAEPSTI--CAGE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.2%;
24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 67; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-712 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 LQKVLPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
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                                                                                                                                                                                                                     201
                                                                                   150
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                                                                                QΥ
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A; Cross-references: EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983
A; Note: the authors translated the codon CAC for residue 569 as Gln
R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Ratt. Acad. Sci. U.S.A. 83; 5644-5648, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A; Reference number: 159078
A; Accession: 159078
A; A; Accession: 159078
A; Molecule type: DNA
A; Molecule type: DNA
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                        #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ripytela, R. BEMBO 7, 1371-1378, 1988 BMS of the murine Mac-1 alpha chain reveals homology with the A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Reference number: S00551; MUID:88312584 A;Accession: S00551 AMID:88312584 A;Accession: S00551 AMID:88312584 A;Accession: S00551 AMID:88312584 A;Residues: 1-1153 AMID:872-2007640. MID:872-20080. DIDN:GABANA79.1: PID:952983
                    F;2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (Pro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30.5ep-1989 #sequence_revision 30.5ep-1991 #text_change 22-Oct-1999 C;Accession: S00551; I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | | | | | | | AP---KEPAIKLRDADVEIFAVGVEDANTELEAIASPPAETHVYTVED-FDAFQRISFE 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                                                                                                                                                                                                                             QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
                                                                                                                                                                                                                                                                                                                                                                                                                                       157 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD---SKDHVFPVNDGFQALQGIIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>..</del>
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                                                                                                                          Length 3124;
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                                                                                                                                                                                                97;
                                                                                                                             7.5%; Score 143; DB 1; 26.1%; Pred. No. 0.011;
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                                                                                                                                                                                            51; Mismatches
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 24.2 nes 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-44 <RES>
                                                                                                                                        Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 FSVEDTYLL 280
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Best Local S
Matches 71
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Gaps

53;

Indels

Length 712;

DB 2; 108; 51

223

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE
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23.2%; Pred. No. 0.016;
ative 56; Mismatches 115;
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Best Local Similarity 23.2
Matches 74; Conservative
                                               :| | |
1151 NVYPCYRL 1158
       SVEDTYLL 280
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J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Trueb, J.; Trueb, B.

Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MVID:92339443
A;Accession: S22916; MVID:92339443
A;Accession: S22916
A;Status: preliminary
A;Reliminary
A;Relimi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
                                                                                                                                                                       A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 1-1747 <GER>
A; Experimental source: embryo skin
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
R; Apte, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175 R;Trueb, J.; Trueb, B. Eur. J. Biochem. 207, 549-557, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F;1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF
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; Pred. No. 0.016;
45; Mismatches 114; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library, March 1992
                                                                                                                                          Reference number: A45974; MUID:93280195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.28;
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Best Local Similarity 25.4%
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        R;Apte, S.S. submitted to the EMBL Data L. A;Reference number: S30085 A;Accession: S30085 A;Molecule type: mRNA A;Residues: 1472-1660 <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :Molecule type: mRNA
:Residues: 1472-1660 <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
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C;Species: Caenorhabditis elegans
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: 842373
R;Smith, A.
Submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1213 DELITFVCETASATCPLVFKDGDKLA-----GFKMMEMFGLVEKEFSAIDGVSMEPGTF 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen alpha 1(XIV) chain precursor, long form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1888 <TRU>
A; Cross-references: EMBL:X70793; NID:9288872; PIDN:CAA50064.1; PID:9288873
R; Waelchli, C.; Trueb, J; Ressler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A; Title: Complete primary structure of chicken collagen XIV.
A; Reference number: S31211; MUID:93185668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.0%; Pred. No. 0.066;
Matches 62; Conservative 44; Mismatches 116; Indels
                                                                                                   submitted to the EMBL Data Library, January 1993
A; Reference number: S78476
A; Accession: S78476
                                                                                                                                                                                                                                                                                             A; Accession: S31211
A; Status: preliminary
A; Molecule type: MRNA
A; Residues: 1-416;1460-1811,1843-1888 <WAE>
A; Cross-references: EMBL:X70793
                                                                    C; Accession: S78476; S31211
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A.Molecule type: mRNA
A.Rosidues: 1.1857 <WAE>
A.Cross-references: EMBL:X70792; NID:g288874; PIDN:CAA50063.1; PID:g288875
A.Mote: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                         collagen alpha 1(XIV) chain precursor, short form - chicken c. Species: Gallus gallus (chicken) c.Species: Gallus gallus (chicken) 17-Apr-1998 #text_change 13-Aug-1999 C.Accession: S31212 R.Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Bur. J. Blochem. 212, 483-490, 1993 A.Title: Complete primary structure of chicken collagen XIV. A;Reference number: S31211; MUID:93185668
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                                                                                                 183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
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                                                                                                                                                             299 MND-----GLSFISSSVII 312
                                                                                                                                                                                      531 VGDPTSQHGKEFLVEDVII 549
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Best Local Similarity 25.04
Matches 62; Conservative
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1910 XI collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-5ep-1996 #sequence_revision 13-5ep-1996 #text_change 21-Jan-2000
C;Accession: 151027
R;Wei, Y; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII col
A;Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII col
A;Reference number: 151027
A;Reference number: 151027
A;Reference number; translated from GB/EMBL/DDBJ
A;Residues: 1-929 cwEI>
A;Residues: 1-929 cwEI>
A;Residues: 1-929 cwEI>
A;Cross-references: EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g632648
A;Cross-references: EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g632648
C;Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology cyRR>
F;155-236/Domain: von Willebrand factor type A repeat homology cyWA3>
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N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; he
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragmen
C;Species: Homo sapiens (ann)
C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000
C;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339; A44628;
R;Mejla, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
Submitted to the EMBL Data Library, March 1993
A;Reference number: S34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                               134 ENROGYRTAS--VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 ADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICAGGGGRREDGGPACYGGFDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMS
                                                     82 FIV---FSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y
                                                                                                                                                                                                                                                                                                                                                                 RQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED
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                                                                                                                                                                                                                                 315 GLVQYSSSVRQEFPLGRFHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 929;
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Best Local S
Matches 57
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A:Residues: 1-496 <JEND-
A:Residues: 1-496 <JEND-
A:Residues: 1-490 <JEND-
A:Rocession: B37929
A:Molecule type: mRNA
A:Residues: 157-290, 'L',292-496 <JE2>
A:Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:g
                                                                         A; Molecule type: DNA
A; Residues: 1-3051 <SMI>
A; Residues: 1-3051 <SMI>
A; Cross-references: EMBL: Z30423; NID: 9458479; PID: 9458485
C; Genetics: SMI : 16673; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
C; Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin t
F; 512-679/Domain: von Willebrand factor type A repeat homology <VWAl>
F; 74-793/Domain: fibronectin type II repeat homology <2Fl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cartilage matrix protein precursor - human (5) Species: Homo Sapiens (man) (2) Species: Homo Sapiens (man) (2) Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000 (2) Accession: A37979; B37979 (B; Jul-1997) (C; Jul-1997) (C; Jul-1997) (C; Jul-1997) (Jul-1997) (Jul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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F;1-22/Domain: signal sequence *status predicted <SIG>
F;23-496/Product: cartilage matrix protein *status predicted <MAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWAl>
F;27-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;73-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;6,344/Binding site: carbohydrate (Asn) (covalent) *status predicted
F;221-238,234-247,249-262/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 128; DB 2; Length 3051;
; Pred. No. 0.18;
31; Mismatches 75; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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A;Cross-references: GDB:127280; OMIM:115437
A;Cross-teferences: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
A;Introns: 32,1: 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%; Score 120.5; DB 2; 25.3%; Pred. No. 0.065; ative 37; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.78;
27.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 64; Conservative
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Best Local Similarity 25,39
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                             Accession: S42373
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A.Pathway: complement alternate pathway
A.Pathway: complement C2; complement factor H repeat homology; trypsin homology;
C; Superfamily: complement C2; complement alternate pathway; duplication; glycoprotein; hyd
C; Reywords: acute phase; complement alternate pathway; duplication; glycoprotein; hyd
C; Reywords: acute phase; complement factor B *tatus experimental <MAT>
F; 26-75/Domain: signal sequence *tatus predicted <GIG>
F; 26-75/Product: complement factor B fragment #status experimental <BAF>
F; 26-25/Product: complement factor H repeat homology <FH1>
F; 103-158/Domain: complement factor H repeat homology <FH2>
F; 268-458/Domain: complement factor H repeat homology <FH3>
F; 268-458/Domain: trypsin homology *status atypical <TRX>
F; 482-752/Domain: trypsin homology #status atypical <TRX>
F; 37-76, 62-98, 103-145, 131-158, 165-205, 191-218, 479-596, 511-527, 599-615, 656-682, 695-725
F; 259-260/Cleavage site: carbobydrate (Asn) (covalent) *status experimental
F; 529-260/Cleavage site: Arg-Lys (complement factor D) *status experimental
F; 526, 576, 699/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 6p21.3-6p21.3 A; Map position: 6p21.3-6p21.3 A; Map position: 6p21.3-6p21.3 A; Map position: 6p21.3-6p21.3 A; Map position: 6p21.3 A; Map position: Map position and position of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march of march o
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-764 <RES>
A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689
A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689
B;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.
Mol. Immunol. 30, 1587-1592, 1993
A;Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic of A;Reference number: 157824; MUID:94067177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-31, Q, 33-764 <RE2>
A; Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922
C; Comment: 292-Cys has a free sulfhydryl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 FERASEQIYYENR-----QGY-RTASVIIALTDG-------ELHEDLFFYSE
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19.6%; Pred. No. 0.43;
tive 63; Mismatches 109;
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A; Molecule type: protein

A; Molecule type: protein

A; Note: binding site for carbohydrate to lysine under artificial conditions

A; Note: binding site for carbohydrate to lysine under artificial conditions

A; Note: binding site for carbohydrate to lysine under artificial conditions

B; Molecule type: A, 153-157, 1984

A; Reference number: A44628; MUID:84158524

A; Accession: A44628

A; Accession: A44628

A; Accession: A44628

A; Accession: B; A; Carbohydrate to lysine under zum Busche

A; Accession: Lottig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche

Immunobiology 188, 221-232, 1993

A; Reference number: IS4409; MUID:94041399

A; Accession: I54409
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A; Residues: 339-509 <CA1>
A; Residues: 339-509 <CA1>
A; Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A; Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
B; Mu, L.; Morley, B.J.; Campbell, R.D.
C; Na, A; 131-342, 1987
A; Title: Cell-specific expression of the human complement protein factor B gene: evidend
A; Reference number: A25971; MUID:87102880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Modecule type: mRNA
A; Residues: 467-546; 550-595; 752-764 <moo>
A; Residues: 467-546; 550-595; 752-764 <moo>
A; Residues: 467-546; 550-595; 752-764 <moo>
A; Residues: 467-546; 550-595; 752-764 <moo>
A; Residues: 467-546; 550-595; 752-764 <moo>
A; Residues: 467-546; 550-595; 752-764 <moo>
A; Note: the authors translated the codon TAC at 519 as Thr; the nucleic acid translation
B; Mole: J. Biol. Chem. 259, 3407-3412, 1984
A; Title: Complete primary structure for the zymogen of human complement factor B.
A; Reference number: A20751; MUID:84161997
A; Reference number: A20751; MUID:84161997
A; Molecule type: protein; mRNA
A; Residues: 26-764 <moo>
A; Molecule type: protein; mRNA
A; Residues: 26-764 <moo>
A; Molecule type: protein; mRNA
A; Molecule type: protein; mRNA
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A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecule type: Drotein
B;Campbell, R.D.; Povrer, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene coding for human complement
A;Reference number: A19947; MUID:83273641
A;Accession: A19947
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R; Christie, D.L.; Gagnon, J.
Biochem. J. 209, 61-70, 1983
A; Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of A; Reference number: A19188; MUID:83204002
A; Contents: the final paper in a series documenting the sequence, glycosylation site,
                                                                                                                                               A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-764 <ms.
A; Residues: 1-764 <ms.
A; Cross-references: EMBL:X72875; NID:9297568; PIDN:CAA51389.1; PID:9297569
A; Cross-references: EMBL:X72875; NID:9297568; PIDN:CAA51389.1; PID:9297569
B; Moods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A; Title: Isolabation of cDNA clones for the human complement protein factor B, a class A; Reference number: A44622; MUID:83039428
A; Accession: A44622
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A; Residues: 1-99 GWUL-
A; Residues: 1-99 GWUL-
A; Cross-references: GB:M15082; NID:g187699; PiDN:AAA59625.1; PID:g553534
A; Cross-references: GB:M15082; Miller, E.J.
R; Niemann, M.A.; Bhown, A.S.; Miller, E.J.
Biochem, J. 274, 473-480, 1991
A; Title: The principal site of glycation of human complement Factor B.
A; Reference number: S14339; MUID:91174758
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A;Residues: 346-764 <CAM>
A;Cross-references: GB:J00125
A;Accession: B19947
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A:Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
C;Complex: type VII collagen is probably a homotrimer
C;Function:
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C;Function:
C;Superfamily: unassigned collagens; animal kunitz-type proteinses inhibitor homology
C;Keywords: coiled collagens; animal kunitz-type proteinse inhibitor homology
C;Keywords: coiled collagens; animal kunitz-type proteins
F;17-1253/Domain: ainal sequence stratus predicted ckNI>
F;17-1253/Domain: ainal sequence stratus predicted ckNI>
F;17-1253/Domain: ainor-terminal nonhelical *status predicted ckNI>
F;17-1253/Domain: dibronectin type III repeat homology ckNI>
F;213-2143/Domain: fibronectin type III repeat homology ckNI>
F;215-2153/Domain: fibronectin type III repeat homology ckNI>
F;216-2153/Domain: fibronectin type III repeat homology ckNI>
F;226-2253/Domain: fibronectin type III repeat homology ckNI>
F;226-2
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Job time: 251 sec
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 2395-2871, 'S, 2873-2944 <RDS
A;Residues: 2395-2871, 'S, 2873-2944 <RDS
A;Cross-references: GB:L06662; NID:9388713; PIDN:AAA89196.1; PID:9388714
B;Christiano, A.M.; Rynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser subs
A;Reference number: A55255; MUID:94224777
A;Contents: annotation
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A; Residues: 'EFR',340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C',
A; Cross-references: DBBJ:D1152; DBBJ:D13694; NID:9453699; PIDN:BAA02853.1; PID:9453699
A; Experimental source: keratinocyte
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R; Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A; Title: Human type VII collagen: CDNA cloning and chromosomal mapping of the gene.
A; Reference number: S16316; MUID:91334380
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A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
                                                                                                                             Collagen alpha 1(VII) chain precursor - human N;Alternate names: procollagen alpha 1(VII) chain S;Species: Nono sapiens (man) C;Species: Nono sapiens (man) C;Date: 04 Nov-1994 #sequence_revision 04-Nov-1994 #text_change 20-Sep-1999 C;Accession: A54849; PH0844; S16316; 156328; A30296; 184686 K;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J. J. Biol. Chem. 269, 20256-20262, 1994 A;Title: Cloning of human type VII collagen: Complete primary sequence of the alphal(VII A;Reference number: A54849; MUID:94327588
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R; Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
I nvest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot A; Reference number: 156328; MUID:93107742
A; Accession: 156328
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A;Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A;Reference number: 148103; MUID:93271985
A;Accession: 184686
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A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
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A;Residues: 815-892,'E',894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:9180914; PIDN:AAA96439.1; PID:9180915
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A;Cross-references: GDB:128750; OMIM:120120
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A; Residues: 1-2944 <CHR>
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5.8%; Score 111.5; E 24.1%; Pred. No. 3.9;
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August 9, 2002, 02:02:44; Search time 523.51 Seconds (without alignments) 4926.614 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 176, App	231,	17, A	13,	15,	6	23,	19,	1, 1	25	21,	11,	186,	300,	1170	٠.		3, A	7	Sequence 11267, A		5, A	Sequence 9, Appli	47,	7, 1
ID	PCT-US02-08253-176	PCT-US02-08253-231	US-10-038-307-17	US-10-038-307-13	US-10-038-307-15	US-10-038-307-9	US-10-038-307-23	US-10-038-307-19	US-10-038-307-1	US-10-038-307-25	US-10-038-307-21	US-10-038-307-11	PCT-US02-08253-186	PCT-US02-08253-300	US-09-629-469A-11705	US-10-047-542-98	US-10-047-542-100	US-10-038-307-3	US-09-918-995-22508	US-09-919-002-11267	US-10-104-047-669	US-10-038-307-5	US-60-373-595-9	US-10-125-540-47	US-10-038-307-7
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US-09-629-469A-3023 US-09-539-800C-19015 US-09-629-469A-4890 US-09-539-31D-12581 US-09-539-31D-72449 US-09-539-31D-77849 US-60-377-240-4089 US-60-377-240-4089 US-60-377-240-4089 US-60-377-240-4089 US-60-377-240-4089 US-60-377-240-4089 US-60-377-240-4089 US-60-377-240-4089 US-10-175-525-12 US-10-116-802-287 US-09-918-995-3407 US-09-918-995-3407 US-09-978-4018-4711 US-09-978-4018-4711
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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Kinoler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAT
FILE REPERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,859
                                                                                                                                                                                                                                                                                                                                Sequence 231, Application PC/TUS0208253 GENERAL INFORMATION:
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Matches 1092; Conservative
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acagecagegteateattgetttgaetgatggagaaeteeatgaagatetettttetat 492
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99.4%; Pred. No. 1.7e-260;
ive 0; Mismatches 6;
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFERENCE: 7853-253-999
CURRENT APPLICANTON NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ 1D NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 956; Conservative
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OzKAVNAK
APPLICANT: Judith, J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and N
FILE REPRENEUR: 7853-233-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASLEEQ for Windows Version 4.0
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99.8%; Pred. No. 7.1e-263
Live 0; Mismatches 2
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Best Local Similarity 99.8
Matches 962; Conservative
                                                                                                                                                               gagagtgaggaaaa 1094
                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-17
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 Compositions and
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10S-10-038-307-15
1 Sequence 15, Application US/10038307
2 GENERAL INFORMATION:
3 APPLICANT: James B. ROTTMAN
3 APPLICANT: Engin OKKAYNAK
4 APPLICANT: Engin OKKAYNAK
5 APPLICANT: Theresa L. O'KEEFE
6 APPLICANT: Theresa L. O'KEEFE
7 TILE OF INVENTION: Tango 197 and Tango 216 Com
7 TILE OF INVENTION: Tango 197 and Tango 216 Com
7 FILE REFERENCE: 7853-253-999
7 CURRENT FILING DATE: 2002-06-28
7 NUMBER OF SEQ ID NOS: 26
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                                      Length
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                                     ore 952.4; DB 7;
ed. No. 1.7e-260;
Mismatches 6;
                                       Score 9
Pred. N
0; Mism
Windows Version
                                      86.3%;
nilarity 99.4%;
Conservative 0
                     sapiens
 for
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 FastSEQ
         ; LENGTH: 1650
; TYPE: DNA
; ORGANISM: HOMO S
US-10-038-307-15
                                              Best Local Sim
Matches 956;
                                        Query Match
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APPLICANT: Theresa L. O'KEFF
APPLICANT: Theresa L. O'KEFF
APPLICANT: Engin OzKAYNAK
TEPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 950; Conservative
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Pred. No. 4.9e-260;
); Mismatches 7;
                                                                                                                    APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: THERESA L. O'KEEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFRENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                       US-10-038-307-9; Sequence 9, Application US/10038307; GENERAL INFORMATION:
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99.38;
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Matches 955; Conservative
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Pred. No. 1.3e-259;
0; Mismatches 1;
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Bugin Ozkarnak
TITLE OF INVENTION: Tango 197 and Tango 216 C
FILE REPERBENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                          and Tango 216
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CORGANISM: Homo sapiens
US-10-038-307-19
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950; Conserv
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US-10-038-307-19
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GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
                                                                                                                                                                                                                                                                     APPLICANT: Theresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and
FILE REFERENCE: 7853-253-999
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; ORGANISM: Homo sapiens
US-10-038-307-25
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Best Local Simi
Matches 952;
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Pred. No. 1.4e-259;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/038,307 CURRENT FILING DATE: 2002-06-28 UNDBER OF SEQ ID NOS: 26 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                      86.0%;
                                                                                            al Similarity 99.9
950, Conservative
                                                      ; NAME/KEY: CDS
; LOCATION: (213)...(1211)
US-10-038-307-1
                                           ORGANISM: Homo sapiens
                              LENGTH: 2272
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Best Local S:
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                                                Compositions and
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                                                                                                               RESULT 10
US-10-038-307-25
Sequence 25, Application US/10038307
Sequence 25, Application US/10038307
GENERAL INCOMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Didith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Commy
FILE REPERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT PILING DATE: 2002-06-28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 1008
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Matches 879; Conservative
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LENGTH: 1623
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US-10-038-307-11
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      aaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatgtgtttccc
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Pred. No. 3.5e-249;
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                                                                                                                                                                                                                                                                      APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Enqin OXKANAK
APPLICANT: Enqin OXKANAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216
CURRENT FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                       and Tango 216
                                                                                                                                                                                                                                                     Sequence 21, Application US/10038307 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.6%;
Best Local Similarity 97.1%;
Matches 950; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-10-038-307-21
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 21
LENGTH: 1047
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Pred. No. 2.3e-236;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4...
LENGTH: 5220
                                                          CT-US02-08253-186
                                                     TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAT
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
PCT-US02-08253-186
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5220;
Length
              Indels
Score 853.4; DB 1;
Pred. No. 3.8e-232;
0; Mismatches 136;
77.3%;
87.3%;
Query Match 77.3
Best Local Similarity 87.3
Matches 935; Conservative
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Pred. No. 3.8e-232;
); Mismatches 136; Indels 0;
                                                                                APPLICANT: Carson-Halter, Eleanor
APPLICANT: St. Carson-Halter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-0
NUMBER OF SEQ ID NOS: 359
NUMBER OF SEQ ID NOS: 359
SOFTWARE: EastSEQ for Windows Version 4.0
                                                                                                                                 Sequence 300, Application PC/TUS0208253 GENERAL INFORMATION:
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Best Local Similarity 87.3%;
Matches 935; Conservative
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PCT-US02-08253-300
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PCT-US02-08253-300
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LENGTH: 5220
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GAPLICANT: OTA, TOSHIO
APPLICANT: OTA, TOSHIO
APPLICANT: ISOGAI, TAKADO
APPLICANT: ISOGAI, TAKADO
APPLICANT: ISOGAI, TAKADO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: SAITO, KAOJI
APPLICANT: SAITO, KAOJI
APPLICANT: SAITO, MARMOTO, JUNICHI
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: WAKAMATSU, AI
APPLICANT: WAKAMATSU, AI
APPLICANT: OTSUIL, TETSUOI
TITLE OF INVENITON: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
FILE REFERENCE: 084335/0123
CURRENT FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 2000-01-11
PRIOR FLIING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
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Sequence 11705, Application US/09629469A
GENERAL INFORMATION:
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                                                                                                                                                Length 1436;
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                                                                                                                                               Score 787; DB 5; I
Pred. No. 1.8e-213;
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    APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: UF 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR PRILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/183,322
PRIOR FILING DATE: 1999-10-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 11705
LENGTH: 1436
                                                                                                                                               71.3%;
99.3%;
                                                                                                                                                               Matches 801; Conservative
                                                                                                 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-09-629-469A-11705
                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                               Query Match
Best Local Similarity
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Search completed: August 9, 2002, 02:03:04 Job time: 10801 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 9, 2002, 01:53:53; Search time 4997.37 Seconds Run on:

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4779.500 Million cell updates/sec

us-09-970-076-1_COPY_104_1207

Perfect score: Sequence: Scoring table:

IDENTITY_NUC Gapox 1.0

21979536 segs, 10817449327 residues Searched:

43959072

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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/cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
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 /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
 /cgn2_6/ptodata/2/pna/US06_COMB.seq:*

<pre>. /cgn2_6/ptodata/2/pna/US6005_COMB.seq:* . /cgn2_6/ptodata/2/pna/US6006_COMB.seq:* . /cgn2_6/ptodata/2/pna/US6007_COMB.seq:* . /cgn2_6/ptodata/2/pna/US6009_COMB.seq:* . /cgn2_6/ptodata/2/pna/US6009_COMB.seq:* . /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*</pre>	Cyptodata/2/pna/US6011_COMB.s 6/ptodata/2/pna/US6012_COMB.s 6/ptodata/2/pna/US6013_COMB.s 6/ptodata/2/pna/US6015_COMB.s 6/ptodata/2/pna/US6015_COMB.s 6/ptodata/2/pna/US6016_COMB.s 6/ptodata/2/pna/US6016_COMB.s		2_6/ptodata/2/ 2_6/ptodata/3/ 2_6/ptodata/3/ 2_6/ptodata/3/ 2_6/ptodata/3/ 2_6/ptodata/3/ 2_6/ptodata/3/ 2_6/ptodata/2/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli	12	176,	Sequence 231, App	S, A	14,	45,	10,	e 10,	10,	10,	Sequence 7, Appl1	æ	æ	œ	~ &	Sequence 11, Appl	-	4357	68, A	204,	988,	204,	68,	988,	988,	~	7637,	Sequence 7309, Ap	628	Sequence 5593, Ap
QI	US-09-970-076-1	213-359-1	US-09-918-715-176	918-715-2	-60	0-30045-1	-	PCT-US99-31025-10	US-09-223-546-10	_	US-09-599-596-10	us-09-970-076-7	PCT-US99-31025-8	US-09-223-546-8	US-09-471-179-8	-09-299-296	US-09-796-753-11	-09-644-871-9	-09-710-281-	-09-329-548A-	-09-419-553-20	-09-516-44	-09-770-155	-09-780-183	-09-833-381	-09-833-382	-09-371-	-09-644-868	-09-644-871-7	-09-649-163-62	US-09-652-121-5593
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% Query Match	100.0	98.8	98.8	98.8	98.8	98.8	98.7	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	85.9	85.9	85.9	85.9	85.9
Score	1104	1090.8	1090.8	1090.8		1090.6	1089.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	947.8	947.8	947.8	947.8	947.8
Result No.	1	7	٣	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Oy 361 catgaaggatttgaaagggccagtgagcagatttattatgaaaacagacaagggtacagg 420 [Oy 661 atogaaattotagoagotgaaccatcaccatatgtgcaggaggtcatttcaagtgc 720	RESULT US-60-213-359-1222 Sequence 1222, Application US/60213359 Sequence 1222, Application US/60213359 GENERAL INFORMATION: APPLICANT: Necreti APPLICANT: Lal, Preeti APPLICANT: Diep, Dinh TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using TITLE OF INVENTION: Dipylnuclectide Sequence Databases, and Single Nucleotide Poly TITLE OF INVENTION: Identified Thereby TITLE OF INVENTION: Identified Thereby TITLE OF INVENTION: Identified Thereby TITLE OF INVENTION: 1000-06-21 CURRENT FILING DATE: 2000-06-21 NUMBER OF SEQ ID NOS: 7924 SOFTWARE: PERL Program SEQ ID NO 1222 LENGTH: 2386 TYPE: DAA CORGANISM: Homo Sapiens FEATURE:
32 947.8 85.9 2401 25 US-09-652-127-7873 Sequence 7873, Ap 347.8 85.9 2401 31 US-09-801-833-7727 Sequence 7877, Ap 347.8 85.9 2401 31 US-09-801-833-7727 Sequence 1727, Ap 357.4 84.9 2397 24 US-09-668-337-188 Sequence 188, App 36 853.4 77.3 520 34 US-09-918-715-186 Sequence 1757, Ap Sequence 1757, Ap 287.4 77.3 520 34 US-09-918-715-186 Sequence 186, App Sequence 300, App 863.8 75.2 2981 75 US-09-918-715-907 Sequence 20845, App 40 803.8 72.8 1402 18 US-09-488-725A-3907 Sequence 3977, Ap 41 803.8 72.8 1609 18 US-09-488-725A-3907 Sequence 3977, Ap 503.8 72.8 1609 18 US-09-488-725A-3907 Sequence 3597, Ap 503.8 72.8 1609 24 US-09-808-725A-3907 Sequence 3597, Ap 503.8 72.8 1609 32 US-09-989-70-706-9 Sequence 250, App 503.8 72.8 1609 32 US-09-970-076-9 Sequence 250, App 503.8 72.8 1609 32 US-09-970-076-9 Sequence 250, App 503.8 72.8 1609 32 US-09-970-076-9 Sequence 250, App 14 787 71.3 1436 36 US-09-970-076-9 Sequence 250, App 15 US-09-970-076-9	RESULT US-09-076-1 US-09-970-076-1 US-09-970-076-1 US-09-970-076-1 US-09-970-076-1 US-09-970-076-1 US-09-970-076-1 Sequence 1, Application US/09970076 GENERAL INCORMATION:	Oy 61 ctggtgctcatctggccaggcaaggggacgcagggggggg

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Pred. No. 1.7e-287;
0; Mismatches 2;
                                                                                                                                                                       EXPRESSION
                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brad St. Catolix
APPLICANT: Bert Vogelstein
TITLE OF INVENTON: ENDOTHELIAL CELL EXPRESSI
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
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Matches 1092; Conservative
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US-09-918-715-176
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                                        Score 1090.8; DB (
Pred. No. 1.2e-287;
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Best Local Similarity 99.8%;
Matches 1092; Conservative
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; Sequence 231, Application US/09918715
; GENERAL INPORMATION:
APPLICANT: Berd St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Menneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESS:
FILE REFERENCE: 1107.00134
CURRENT APPLICATION UNDHER: US/09/918,715
CURRENT APPLICATION NUMBER: 06/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-04-11
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ORGANISM: Homo sapiens
US-09-918-715-231
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LENGTH: 5540
TYPE: DNA
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Query Match
Best Local Similarity 99.8
Matches 1092; Conservative
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FILE REFERENCE: PS708CT
CURRENT APPLICATION NUMBER: PC7/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEO ID NOS: 201
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; APPLICANT: Human Genome Sciences, Inc.
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Matches 1093; Conservative
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APPLICANT: Bradley, Kenneth A.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960.296, 977.5
CURRENT PELLING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 06/251,481
PRIOR APPLICATION NUMBER: 06/251,481
PRIOR APPLICATION NUMBER: 07.51
NUMBER OF SEO ID NOS: 10
NUMBER OF SEO ID NOS: 10
                                                                                                                        Sequence 5, Application US/09970076 GENERAL INFORMATION:
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99.8%;
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SEQ ID NO 5
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LOCATION: (14
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Protein:
FILE REFERENCE: PS708PCT; CURRENT APPLICATION NUMBER: PCT/US00/30045; CURRENT FILING DATE: 2000-11-01; PRIOR FILING DATE: 1999-11-05; PRIOR PILING DATE: 1999-11-05; PRIOR FILING DATE: 2000-06-30; PRIOR FILING DATE: 2000-06-30 3; Mismatches Ö Ö Ü or or or or or NAME/KEY: SITE
LOCATION: (2083)
CTHER INFORMATION: n equals a,t,9,
PCT-US00-30045-45 equals a,t,g, a,t,g, Query Match
Best Local Similarity 99.4%;
Matches 1090; Conservative n equals n equals SEO ID NOS: 201 Patentin Ver. 2.0 n equals ORGANISM: Homo sapiens NUMBER OF SEO ID NOS: SOFTWARE: Patentin Ve SEQ ID NO 45 ū NAME/KEY: SITE LOCATION: (2079) OTHER INFORMATION: NAME/KEY: SITE LOCATION: (10) OTHER INFORMATION: LOCATION: (2075) OTHER INFORMATION: INFORMATION: (2070)NAME/KEY: SITE NAME/KEY: SITE LOCATION: OTHER INFO TYPE: DNA 586 121 181 346 241 406 301 466 361 421 Dp qq δ g Óλ οy g Qγ Ω g δy 8 δy δ

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TITLE OF INVENTION: SECRETED PROTEINS AND
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Pred. No. 5e-249;
); Mismatches
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TITLE OF INVENTION: SECRETED PROTEINS AND NUC;
TITLE OF INVENTION: ENCODING THEM
TITLE OF INVENTION: ENCODING THEM
TITLE OF INVENTION: ENCODING THEM
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT APPLICATION NUMBER: PCT/US99/31025
EARLIER PELLING DATE: 1998-12-33
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 10
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Best Local Simi
Matches 950;
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LENGTH: 999
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                             DB 16;
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                             Score 949.4; DB 1
Pred. No. 5e-249;
0; Mismatches
                             86.0%;
nilarity 99.9%;
Conservative C
              Homo sapiens
                                  Similarity
                             Query Match
Best Local Simi:
Matches 950; C
          ; TYPE: DNA
; ORGANISM: HOI
US-09-223-546-10
 SEQ ID NO 10
LENGTH: 999
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Pred. No. 5e-249;
0; Mismatches 1
                                          Sequence 10, Application US/09471179;
GENERAL INFORMATION:
APPLICANT: HOltzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUC
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
                                                                                                                            NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 999
LENGTH: 999
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99.9%;
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Best Local Similarity 99.9
Matches 950; Conservative
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CORGANISM: Homo sapiens
US-09-471-179-10
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99.9%; Pred. No. 6.8e-249;
ive 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TILE OF INVENTION: Anthrew Toxin Receptor FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2001-10-03
FRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
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Matches 950; Conservative
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US-09-970-076-7
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US-09-970-076-7
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING J
FILE REFERENCE: 09404/066010
CURRENT APPLICATION NUMBER: US/09/599,596
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH. 999
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Pred. No. 5e-249;
0; Mismatches 1; Indels 0;
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Sequence 10, Application US/09599596
GENERAL INFORMATION:
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Best Local Similarity 99.99
Matches 950; Conservative
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US-09-599-596-10
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceticals, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND NUC
TITLE OF INVENTION: BECODING THEM
FILE REFERENCE: 7853-173-28
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT FILING DATE: 1999-12-23
EARLIER REDIGATION NUMBER: 09,723,546
EARLIER FILING DATE: 1998-12-30
SOFTWARE: FastSEQ for Windows Version 4.0
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PCT-US99-31025-8
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LENGTH: 2272
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                                  Score 949.4; DB 1
Pred. No. 7e-249;
1; Mismatches 1
                                            ;
                                  86.0%;
99.9%;
                                             Conservative
        ; NAME/KEY: CDS
; LOCATION: (213)...(1211)
PCT-US99-31025-8
sapiens
                                  Query Match
Best Local Similarity
Matches 950; Conserv
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ORGANISM: FEATURE:
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                                                                                                                                                                                   Sequence 8, Application US/09471179
GENERAL INFORMATION:
APPLICANT: HOLIZMAN.
APPLICANT: HOLIZMAN.
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM FILE REPERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT APPLICATION NUMBER: 099/23,546
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGHAL 2272
                                273 ctggtgctcatctgcgccgggcaagggggacgcagggaggatgggggtccagcctgctac
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Larity 99.9%; Pred. No. 7e-249;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (213)...(1211)
US-09-471-179-8
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Best Local Similarity
Matches 950; Conserv
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ORGANISM: HOMO
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                                                            APPLICANT: HOLICAND.

APPLICANT: HOLICAND.

TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM FILE REFERENCE: 09404/06601

CURRENT APPLICATION NUMBER: US/09/223,546

CURRENT FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 8
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Indels
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Pred. No. 7e-249;
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                                               Sequence 8, Application US/09223546 GENERAL INFORMATION:
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; LOCATION: (213)...(1211)
US-09-223-546-8
                                                                                                                                               ORGANISM: Homo sapiens
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                                        US-09-223-546-8
                                                                                                                                        TYPE: DNA
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Sequence:

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ADDRESEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
Z119-22313-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
              REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFRAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
FILING DATE: 26-MG-1991
ATTORNEY/AGEN: INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
2252
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2881
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2472.460 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-232-463-14
US-08-728-323A-1
US-08-757-669A-20
US-09-230-371A-20
US-09-230-371A-20
US-08-321-615A-3
US-08-321-777-3
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US-08-321-615A-1
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US-08-377-690-1
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US-08-477-989-07-1
US-09-189-607-1
US-09-378-907-1
US-08-487-427-25
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Maximum Match 100%
Listing first 45 summaries
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                                                                       689 ccatatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggcttccgacatgccc 748
                                         Gaps
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                                         ;
0
     ch 4.3%; Score 47; DB 1; Length 7218; 1 Similarity 6.7%; Pred. No. 0.00014; 26; Conservative 199; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: 52
CORRESPONDENCE FOLGY & Lardner
STREET: Folgy & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttatcaaggaggtccctccacccctgcc 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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Patent No. 5670367
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 14:
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ZIP: 22313-0299
          Query Match
Best Local Similarity
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                                                                                                                                                           Length 7218;
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                                                                                                                                                                            1 Similarity 6.8%; Pred. No. 0.0094;
27; Conservative 198; Mismatches 174; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-728-323A-1/c
; Sequence 1, Application US/08728323A
; Patent No. 5948676
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Boseo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                                                   Query Match 3.8%;
Best Local Similarity 6.8%;
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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CLASSIFICATION: 435
                                                                                        ; CLONE: pTZgpt-F1s
US-08-232-463-14
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: U.S.A.
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New York
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US-08-757-669A-20
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Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Bohenzky, Roy A.
APPLICANT: Bohenzky, Roy A.
APPLICANT: Bediman, Isldore S.
APPLICANT: Bediman, Isldore S.
APPLICANT: HONCE, PETICE S.
APPLICANT: HONCE, PETICE S.
APPLICANT: HONCE, PETICE S.
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Pred. No. 0.11;
0; Mismatches 91; Indels 0
                                                   0575/52268/JPW/MSC/SKS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
              NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3489 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                      3.48;
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 50.3'
Matches 92; Conservative
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; LOCATION: 1..3
US-08-728-323A-1
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GENERAL INFORMATION:

APPLICANT: Bohenzky, Roy A

APPLICANT: Moore, Patrick S

APPLICANT: Moore, Patrick S

TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 45185-6-PCT-US

CURRENT PALICATION NUMBER: PCT/US97/13346

PRIOR FILING DATE: 1999-11-17

PRIOR FILING DATE: 1997-07-22

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver: 2.0
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50.3%; Pred. No. 0.52;
tive 0; Mismatches 91;
                                                                                                                                                  Score 37.4; DB 4;
pred. No. 0.52;
0; Mismatches 91;
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; Sequence 20, Application US/09230371A
; Patent No. 6348586
           LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                      Query Match 3.4%;
Best Local Similarity 50.3%;
Matches 92; Conservative (
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LENGTH: 32207
                                                                                                       US-08-757-669A-20
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; Sequence 3. Application US/07882202A
; Patent No. 5374617
; Patent No. 5374617
; GENERAL INFORMATION:
; APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Treatment of Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
; STREET: Lall Elm Street, Suite 4500
; CITY: Dallas
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                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-10
EARLIER FILING DATE: 1999-06-10
EARLIER FILING DATE: 1999-06-10
EARLIER FILING DATE: 1999-06-10
SEALIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1998-08-31
SEALIER FILING DATE: 1998-08-31
NUMBER OF SEO ID NOSS: 544
SOFTWARE: FREESEQ FOR WINDOWS VEFSION 3.0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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50.8%; Pred. No. 0.035;
Live 0; Mismatches 64;
; Sequence 368, Application US/09385982
; Patent No. 6262334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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Best Local Similarity
Matches 66; Conserv
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US-07-882-202A-3
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928 gtcatcatcaccaccacacactgttctgacggttccatcctggccatcgcctgctgatc 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2%; Score 35.2; DB 1; Length 1440; 62.5%; Pred. No. 0.32; 1ve 0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Coding portion of human factor VII cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION S14
PRICA PPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: HANSEN, EUGENIA S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290C
                                                                   OMRF B34290CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Richards, Medlock & Andrews STREET: 1201 Elm Street, Suite 4500 CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFRENCE/DOCKET NUMBER: 31,966
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMATION FOR SEQ 10 NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDMESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-008-321-777-3
Sequence 3, Application US/08321777
; Patent No. 5504067
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.29
Best Local Similarity 62.59
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COCATION: 36.1433
CTHER INFORMATION:
CTHER INFORMATION:
US-08-021-615A-3
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Texas
                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
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APPLICANT: Moorissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with an Activator of
TITLE OF INVENTION: FVII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.2%; Score 35.2; DB 1; Length 1440; ilarity 62.5%; Pred. No. 0.32; Conservative 0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 36.1433
OTHER INFORMATION: /note= "Coding portion of human
OTHER INFORMATION: factor VII cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: 15270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,615A
FILING DATE: 19-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,202
FILING DATE: 13-MAY-1992
                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 0MRF B34290
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECRAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  988 ctgttcctgctcctagccctggctctcc 1015
APPLICATION NUMBER: US/07/882,202A FILING DATE: 13-MAY-1992 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08021615A Patent No. 5504064 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo say
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-021-615A-3
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| Sequence 13, Application US/09009656 | Patent No. 6132730 | Patent No. 6132730 | Patent No. 6132730 | Patent No. 6132730 | CENERAL INFORMATION: Thorpe, Philip E. APPLICANT: Thorpe, Philip E. APPLICANT: Gao, Boning | APPLICANT: Gao, Boning | TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA | TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR | TITLE OF INVENTION: TREATMENT | NUMBER OF SEQUENCES: 27 | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COAGULATION AND TUMOR | COA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: CONCULTENTLY Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.2; DB 3;
Pred. No. 0.32;
0; Mismatches 33;
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APLICATION NUMBER:
FILING DATE: 27-MAR-1997
PRIOR APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,920
FILING DATE: 27-JAN-1997
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988 ctgttcctgctcctagccctggctctcc 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UTSD:537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Arnold, White & Durkee P.O. Box 4433
                                                                                               UTSD:536
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REGISTRATION NUMBER: 41,071
REFERENCE,DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/474-7577
                          NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.2%;
Best Local Similarity 62.5%;
Matches 55; Conservation
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
COUNTRY: USA
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US-09-009-217-13
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US-09-009-656-13
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Sequence 13, Application US/09009217
Patent NO. 6132729
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: CCMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Annold, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSEON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 36..1433
CTHER INFORMATION: /note= "Coding portion of human or there information: factor VII cDNA"
US-08-321-777-3
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COMPUTER REABBLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING DATE: CONCULTENTLY HERWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICATION NUMBER: US 60/042,427
PILING DATE: 27-MAR-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
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TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INPORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.59
watches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-009-217-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: F
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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/product= "Tissue Factor"
/note= "Coding portion of human factor VIII cDNA"
/citation= ([1])
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1440;
                                                                                                                                                                                                                                                                                                                  33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bragengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                 Query Match 3.2%; Score 35.2; DB 5; Best Local Similarity 62.5%; Pred. No. 0.32; Matches 55; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/062,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988 ctgttcctgctcctagccctggctctcc 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       957 CIGCACCAGCCCGIGGICCTCACIGACC 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13952-8-4
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ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: PARTELES, 54even W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13955
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9601
TELEPHONE: 206-467-9601
SEQUENCE CHARACTERISTICS:
LENTH: 2422 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08475845 Patent No. 5788965 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berkner, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
NAME/KEY: CDS
LOCATION: 36..1433
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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US-08-475-845-1
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Pred. No. 0.32;
0; Mismatches 33; Indels 0
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APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or
TITLE OF INVENTION: FVII Activator for Blood Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTORNEY. PEB-1993
ATTORNEY. AGENT INFORMATION:
NAME: Trujillo, Doreen Y.
REGISTRATION NUMBER: 35,7719
REFERENCE/DOOKET NUMBER: 27,7719
REFERENCE/DOOKET NUMBER: 21,7719
REFERENCE/DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 19930512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Richards, Medlock & Andrews
1201 Elm Street, Suite 4500
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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   INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                  Query Match 3.2%;
Best Local Similarity 62.5%;
Matches 55; Conservative
                             SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-656-13
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ORIGINAL SOURCE:
ORGANISM: Homo sapi
TISSUE TYPE: Blood
FEATURE:
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CITY: Dallas
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COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
PCT-US93-04493-3
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Gaps

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Score 35.2; DB 1; Length 2422; Pred. No. 0.46; 0; Mismatches 33; Indels 0

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| NAME/KET: CDS | LOCATION: 28.11420 | COCATION: 28.11420 | COCATION: OTHER INFORMATION: /codon_start= 28 | COPHER INFORMATION: /product= "Factor VII" US-08-327-690-1
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Best Local Similarity 62.5%;
Matches 55; Conservative
                   MOLECULE TYPE: CDNA HYPOTHETICAL: N
TOPOLOGY: linear
                                                         ANTI-SENSE: N
FEATURE:
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                                                                                                 NAME/KEY: CDS
LOCATION: 28..1420
OTHER INFORMATION: /codon_start= 28
OTHER INFORMATION: /product= "Factor VII"
US-08-475-845-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Hegengaard, Claus
TITLE OF INVENTION: Modified Factor VII
WIMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/065,725
FILING DATE: 28-FEB-1991
CLASSIFICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION NUMBER: 07/662,920
                                                                                                                                                                                                                                                                                                                                                                                                              988 ctgttcctgctcctagccctggctctcc 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATMELE, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPRA: 415-543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2422 base pairs
TYPE: nucleic acid
"""DANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
2IP: 94105-1492
COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFFWARE: PatentIn Relean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08327690 Patent No. 5817788
          linear
                         MOLECULE TYPE:
HYPOTHETICAL:
                                                                 ANTI-SENSE: N
FEATURE:
        TOPOLOGY:
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BB649806 BB649806
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BC95199 CM4-CT062
BF531402 60201692
BF531402 60203692
BM150243 TCAAP9089
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AU139036 AU139036
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                                                                                                                                                                                         AI750523 cn03g04.x
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BM423073 PLATEL G1
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A1905553 CM-BT092-
AV667876 AV667876
AA037321 zc52b09.r
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BG999787 MR3-HN005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1063)
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1 (bases 6 to 1063)
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2 (contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Emall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                     B1869089
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AW106196
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VERSION
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SOURCE
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
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  RESULT
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BG323538 602422195
AIO84806 0280d12.x
BE146135 MRO-HT020
BE146135 MRO-HT020
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5315.202 Million cell updates/sec
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                                                                                                                                                                                                                                                                                              8, 2002, 23:02:53 ; Search time 2803.4 Seconds
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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em_gss_inv:*
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Maximum DB seq length: 200000000
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/nab_nooped brain, lung, testis; Vector:
    pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA
    source annonymous pool of male brains, age range 23-27; 1
    male lung, age 27; and 1 male testis, age 69. Library is
    oligo-dr primed and directionally cloned (ECORV site is
    elserroyed upon cloning). Average insert size 1.8 kb,
    insert size range 1-3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    Gruber (Invitrogen). Research Genetics tracking code
    code. 202 c 245 g 205 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                              ggcggatttgacctgtacttcattttggacaaatcaggaagtgtgctgcaccactggaat
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Plate: LLAM11448 row: n column: 07
High quality sequence stop: 804.

1. .878
                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                62.0%; Score 684.6; DB 10; 95.1%; Pred. No. 2.9e-176; iive 0; Mismatches 29;
                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179974"
/clone_Ilb="NIH_MGC_115"
/lab_host="DH108"
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Best Local Similarity 95.1
Matches 783; Conservative
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                                      3;
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11H-WGC http://mgc.nci.nih.gov/.
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                                                            atggccacggcggagcggagagccctcggcatcggcttccagtggctctctttggccact 60
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                                                                                                                           Length 1063;
                                       Indels
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Pred. No. 3.3e-178;
1; Mismatches 18;
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                62.7%;
96.6%;
                                         Matches 739; Conservative
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BI823853
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                             Similarity
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                 Query Match
Best Local
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SOURCE
ORGANISM
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Length 878; Indels 116 120 236

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Kato, H., Kawai, J., Kojima, Y., Kouda, M., Koya, S.,
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D.,
Schrimi, L., Shibata, K., Saho, H., Sasaki, D.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I.,
Hayashizaki, Y., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter
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GLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYE
FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTRFRGWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB28591.1"
/db_xref="G1:12850100"
/translation="MKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENS
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KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV
DRVLCSFKINDSVTLNEKPFAVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSV
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
PRE: Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source key:Q9NVP3, evidence:ISS FIS, CLONE NT2RP2005000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acaaccttaatgaaactgacagaagacagagacaaatccgtcaaggcctagaagaactc 327
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Pred. No. 2.7e-175;
0; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="MGD:MGI:1904936"
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homolog to CDNA FLJ10601
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/orqanism≂"Mus musculus"
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/clone="2810405N18"
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5 (bases 1 to 1614)
5 Adachi,J., Alzawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
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High-efficiency full-length cDNA cloning
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. 725
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/db_xref="taxon:9666"
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM810 row: n column: 19 High quality sequence stop: 711.
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420

360 473 540

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ECORI; CDNA made by oligo-dr priming. Directionally
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adaptor: GGCACGAG(G). Size=reslected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
)9 a 189 c 240 g 181 t l others
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602402412F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:4544691 5',
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 820)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory ,
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Lncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1228 row: h column: 04
High quality sequence stop: 815.
Location/Qualifiers
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                             teetttattgtttteteeaeeegaggaacaaeettaatgaaaetgacagaagacagagaa 300
                                                           654 AAAAGATCTCATGAGACAAGTTTGGCC--GGATGCGGACAGTAAGGATCATGTGTATCCC 711
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TITLE
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/clone="INAE.MCG_14"
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/tlssue_type="renal cel
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I (bases 1 to 963)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L (npublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1276 row: c column: 21

High quality sequence stop: 718.
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601 CAGCATGAACGATGGCCTCTTTTTATCTCCAGTTCTGTCATCATCACCAGCAACACTTG 660
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Pred. No. 5.4e-149;
0; Mismatches 20;
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Best Local Similarity 96.3
Matches 621; Conservative
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ORIGIN

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/organism="Homo sapiens"
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Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM1230 row: a column: 15

High quality sequence stop: 659.

Location/Qualifiers
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Pred. No. 8.3e-121;
0; Mismatches 5;
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Best Local Similarity 98.1%;
Matches 530; Conservative
                                                                                                                                                                               .964
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 964)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                  DB 10;
                                                              Score 582.6; DB 10
Pred. No. 2.3e-148;
                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG281831.1 GI:13030757
                                                                    52.8%;
96.1%;
                                                                                                        Matches 683; Conservative
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BG281831
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                                                                                       Similarity
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                                                                        Query Match
Best Local
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L' Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://magqe.llnl.gov

Plate: LLAW8756 row: p column: 04

High quality sequence stop: 573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

148 c 173 g 144 t
601220816F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3589875 5'
                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTTCTGCCAGGAGAGACACTTACATGCACGAAGGATTTGAGAGGGCCAGTGAGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 447.4; DB 10; Length 638; Pred. No. 2.1e-111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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                                                BE369415.1 GI:9314778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.5%;
85.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543; Conservative
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                mRNA sequence.
BE369415
                                                                                  house mouse
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ORIGIN
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/db_xref="taxon:9666"
/clone_lib="Hr0209"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from OreSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
Enail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-MRO-HT0209-280
300-106-909&t3=2000-03-286t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence start: 21
High quality sequence story: 513.
                                                                                                                                                                                                                                                                                                                                                                                                               BE146084 513 bp mRNA linear EST 21-JUN-2000 MRO-HT0209-280300-106-909 HT0209 Homo sapiens cDNA, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 513)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., Bordin, S., Costa, F.F.,

Nagal, M.A., Ad Slivay, Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M. Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                            691
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                                                                                                                                                          751
tcatccactcaattttgaagaagtcctgcatcgaaattctagcagctgaaccatccacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                    38.1%; Score 420.4;
                                                                                                                                                                                                                                                                                                  599 ATGTGGACAGGGCCCCTGGGGTCTAAATAATGA 631
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BE146084.1 GI:8608808
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 465)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.
                          // Organism="Homo sapiens"
/db_xref="taxon:9606"
/dc_stage="Adult"
/dc_stage="Adult"
/dc_stage="Adult"
/note="Organ: head_neck; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
Site_1: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
Site_1: SmaI; A mini-library was made by cloning products
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDMA amplification were performed under
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Pred. No. 5e-104;
0; Mismatches 1;
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131 c 162 g 115 t
Location/Qualifiers
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99.8%;
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Matches 421; Conservative
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BE145958/c
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1 (bases 1 to 542)

Diass Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0209-280 3300-106-b03&t3=2000-03-28&t4=1)
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MRO-HT0209-280300-106-b03 HT0209 Homo sapiens CDNA, mRNA sequence.
BE146075.1 GI:8608799
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                         atggccacggcggagagcgctcggcatcggcttccagtggctcttttggccact
                                                                                        ATGGCCACGGCGGAGCGGAGGCCTCGGCATCGGCTTCCAGTGGCTCTTTTGGCCACT
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                         Indels
          4.9e-104;
                            Mismatches
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High quality sequence stop: 131
          No.
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Email: asimpson@ludwig.org.br
          Pred.
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          99.88;
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        Best Local Similarity
Matches 421; Conserv
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Matches 397; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0020g"
/dev_stage="Adult"
/dev_stage="Adult"
/note="organ: head_neck; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Site_1: Site_l: Smal;
Site_1: Smal; A mini-library was made by cloning products
for income ORESTES PCR (U.S. Letters Patent application
No. 196,116 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
low stringency, conditions."
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                                                                                                                                                      Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=MRO-HT0209-100
100-103-f09&t3=2000-01-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
Location/Qualifiers
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Pred. No. 2e-98;
0; Mismatches 12; Indels 0
                    (7), 3491-3496 (2000)
                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                    97
sequence tags
Proc. Natl. Acad. Sci. U.S.A.
20202663
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Best Local Similarity 97.1%;
Matches 407; Conservative
                                                                                                                           rel: +55-11-2704922
                                                                                                                                            Fax: +55-11-2707001
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/organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone_lib="HT0209"
/dev_stage="Adult"
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Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORFESS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
14 a 147 c 121 g 115 t
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                                             1 (bases 1 to 487)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G. H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Slmpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                             Paulo-SP,
                                                                                                                                                                                         Shorgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.6e-94;
0; Mismatches 2;
                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: puc 18 forward
High quality sequence start: 30
High quality sequence stop: 487.
Location/Qualifiers
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Length 539;

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human.
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Query Match
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                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 539)
Marra,M., Hillier,L., Mucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The Washin-NcI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.lln.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
360
                100 CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
 caaatccgtcaaggcctagaagaactccagaaagttctgccaggaggagacacttacatg
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/organism="Mus musculus"
/strain="C57BL/64"
/db_xref="taxon:10090"
/clone="IMAGE:439399"
/clone=lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="la15-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                             361 catgaaggatttgaaagggccagtgagcagatttattatg 400
                                                                           quality sequence stop: 454
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Putative full length read
vector to vector length is 709
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                                                                                                                                                                                                                                                                       house mouse.
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JOURNAL
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 693)
NIH-WGC http://mgc.ncl.nih.gov/.
NIH-WGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                         Gaps
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                                                                                                                                                                                                                                                                                                                                             484 gagaggaggctaataggtctcgagatcttggtgcaattgtttactgtgttggtgtgaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 gccagcgtcatcattgctttgactgatggagaactccatgaagatctctttttctattca
                                         ó;
                                            Indels
Score 381.2; DB 9
Pred. No. 2.6e-93;
0; Mismatches 63
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/db_xref="taxon:9606"
/clone="IMAGE:4560214"
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      34.5%;
86.9%;
                         Best Local Similarity 86.9
Matches 419; Conservative
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Contact: Robert Strausberg, Ph.D.
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Best Local Simi
Matches 376;
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          /tissue_type="remail cell adenocarcinoma"
/lab.host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5/
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1: 8Rb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia: Eutheria: Primates; Catarrhini: Hominidae; Homo.

1 (bases 1 to 554)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                        34.1%; Score 376.4; DB 10; Length 693; ilarity 91.9%; Pred. No. 5.9e-92; Conservative 0; Mismatches 31; Indels 12;
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clone_lib="NIH_MGC_14"
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Unpublished (1997)
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Matches 487;
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TITLE
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Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Seq primer: -40ml3 fwd. Er from Amersham
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                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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'product= "Mature human secreted

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AAD05300-AAD05379 represent CDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. CC AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing. CC treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mitations in the new genes. Specific uses are described for each of the colliferative disorders. For the diagnosis or treatment of an include developing products for the diagnosis or treatment of conflictative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, allergies, neurological disorders (e.g., Alzheimer's disease, allergies, neurological disorders (e.g., Alzheimer's disease, skin disorders, gastrointestinal disorders, pregnancy related disorders, and infections. The proteins can also be used to aid wound clasorders, and infections. The proteins can also be used to aid wound clasorders, and infections. The proteins can also be used to aid wound clasorders, and infections the proteins can also be used to aid wound clasorders, and infections to regenerate tissues, to identify their computation or parametry tissues, to regenerate tissues, to identify their comparation and an encouration and encouration or promormation or propertine of primary tissues, to regenerate tissues, to identify their comparation.
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                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid molecules encoding 28 human secreted proteins for sposing, preventing, treating or ameliorating medical conditions and
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99.6%;
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30-JUN-2000; 2000US-0215133.
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ADD05300-AADD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01544-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, the genes and their secreted proteins are useful for preventing. The genes and their secreted proteins e.g., by protein or gene therapy pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the second of the inspecience of mutations in the new genes. Specific uses are described for each of the second of the inspecience of mutations in the new genes. Specific uses are described for each of the second include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental about an information allergies, hematopoietic disorders, diseases of the immune system, abnormalities, hematopoietic disorders, schizophrenia, asthma, allergies, neurological disorders, schizophrenia, asthma, allergies, neurological disorders, schizophrenia, asthma, cardiovascular disorders, angiogenic disorders, kidney disorders, endocrine disorders, and infections. The proteins can also be used to aid wound
                               Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; anglogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; mifection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19; ss.
                                                                                                                                                                                                                                                                                                                                                                                         /product="Human secreted protein"
/transl_except= (pos:688..690, aa:Xaa)
/transl_except= (pos:1123..1125, aa:Xaa)
/transl_except= (pos:1156..1158, aa:Xaa)
/transl_except= (pos:1267..1269, aa:Xaa)
/note= "Xaa equals any of the twenty naturally ocurring
L-amino acids"
Human secreted protein-encoding gene 4 cDNA clone HWLFR02, SEQ ID NO:45
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used as food additives or preservatives -
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healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g. radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumat arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like actime, graft versus host diseases, rhematoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease,
                                                                                                                        tgtccagcgcctatcttaaaagaagttggcatgaaagctgcactccaggtcagcatgaac
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chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachaxia and autoimmune diseases e.g. mysathemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO 128, 137, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
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                                                                                                                                                                                                                    Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 other;
                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                        Score 949.4; DB 21
Pred. No. 2.5e-280;
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                        cellular disorders can be treated.
                                                                                                                                                                                                                                                                          86.0%;
99.9%;
                                                                                                                                                                                                                                                                                                         Conservative
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950; Conserv
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data for this patent did not form part of the printed
            Note: The sequence specification.
                                                                           Ouery Match
Best Local Similarity
Matches 805; Conserv
                                           Sequence 1402 BP;
  S disorders.
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            1052
                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokactic; thrombolytic; drug screening; arthritis; inflammation;
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tgtccagcgcctatcttaaaagaagttggcatgaaagctgcactccaggtcagcatgaac
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Zhang J;
                                                                                       gatggcctctctttatctccagttctgtcatcatcaccaccacacactgt 951
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Yang Y,
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Xue AJ,
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                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 3907
                                                                                                                                                       BP
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-065319.
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25-APR-2000; 2
09-JUL-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
                                                                                                                                                                                                                                                                                                     leukaemia; ss
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Wang J, V
Zhao QA,
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                                           Length 1402;
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                                                                        Indels
360 A; 354 C; 399 G; 289 T; 0 other;
                                           DB 22;
                                                                        2
                                         Score 803.8; DB 22
Pred. No. 8.8e-236;
0; Mismatches 2;
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                                         72.8%;
ilarity 99.8%;
Conservative
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ctggtgctcatctgcgccgggcaagggggacgcagggaggatgggggtccagcctgctac

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The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polypucleotides are useful
c in gene therapy. A composition containing a polypeptide or polynucleotide
c in gene therapy. A composition containing a polypeptide or polynucleotide
c the invention may be used to treat diseases of the peripheral nervous
c system, such as peripheral nervous injuries, peripheral nervous
c calised neuropathies and central nervous system diseases, such as
localised neuropathies and central nervous system diseases, such as
localised neuropathies and Shy-Drager Syndrome. Other uses include the
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
lateral sclerosis, enclytites such as: Immune system suppression,
c attinisation of the activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
c N. S. disorders.
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                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
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tu C, Xue AJ,
Drmanac RT;
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Goodrich R,
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2000US-052317.
2000US-0598042.
2000US-0629812.
2000US-0653450.
2000US-0653450.
2000US-0653450.
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Wang Z, Wehrman T,
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                           (first entry)
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P-PSDB; AAM38976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153312-A1.
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19-OCT-2000;
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primer; detection; diagnosis; antisense therapy; gene therapy;
Human cDNA sequence SEQ ID NO:11705.
                                          BP.
                                          AAH14331 standard; cDNA; 1436
                                                                                                                                                                      99JP-0248036.
                                                                                                                                                        2000EP-0116126
                                                                       (first entry)
                                                                                                                                                         28-JUL-2000;
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                                                                                                                                                                      29-JUL-1999;
27-AUG-1999;
                                                                                                                 Homo sapiens
                                                                      26-JUN-2001
                                                                                                                                            07-FEB-2001
                                                                                                  Human;
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                              RESULT
AAH14331
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Gaps

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Indels

Query Match
72.8%; Score 803.8; DB 22;
Best Local Similarity 99.8%; Pred. No. 9.5e-236;
Matches 805; Conservative 0; Mismatches 2;

Length 1609;

Ωp δ

ctggtgctcatctgcgccgggcaaggggacgcagggaggatgggggtccagcctgctac 120

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Wang

Ren F, W Zhang J;

Qian XB, Yang Y,

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treating disorders

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682 900 742 9 802 720 862

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cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse; ds.
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                                                                                                       563 acagctagcgtcatcattgctttgactgatggagaactccatgaagatctctttttctat
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                                                               acagccagcgtcatcattgctttgactgatggagaactccatgaagatctcttttctat
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/product= TANGO 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA47479 standard; cDNA; 4417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0223546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holtzman DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-2000
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                                                                                                                                                                                                                                                                                                                                   501
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                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an Oilgo-dr primer and an Oilgonucleotide comprises one of
to the Complementary Strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
collygonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oilgonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide complementary to a
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide complementary to a
coligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence, where the
coligonucleotide comprises at useful for synthesising polynucleotides,
the 5'-end sequence is selected from those defined in
the specification. The primers are useful for synthesising polynucleotides,
condacterion and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAS. The primers allow obtaining of the full-length
condacterion and/or diagnosis of the abnormality of the full-length
condacterion and/or are present human cDNA sequences; AAB0316 to AAH13628 and
AAH13633 to AAH13632 to AAH13632 to AAH13632
condacterion and/or diagnosis of added sequences; and AAH13639 to AAH13630
condacterion and condacterion and sequences; and AAH13630 to AAH13630
condacterion and condacterion and sequences; and AAH13630 to AAH13630
condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterion and condacterio
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                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catgaaaggatttgaaagggccagtgagcagatttattatgaaaacagacaagggtacagg 420
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                                                                                                                                 Saito K, Y. Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1436 BP; 375 A; 349 C; 401 G; 311 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 787; DB 22;
Pred. No. 1.3e-230;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 11705; 2537pp + CD ROM; English.
                                                                                                                                                      Nagai K,
                                                                                                                              Hayashi K,
A, Nagai K
                                                                                                                                 hikawa T,
Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                              Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.3%;
99.3%;
                  02-MAY-2000; 2000JP-0183767. 09-JUN-2000; 2000JP-0241899.
2000JP-0118776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         801; Conservative
                                                                                      (HELI-) HELIX RES INST
                                                                                                                                                   Ishii S, Sugiyama T,
                                                                                                                                                                                                  WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                              Isogai T,
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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셤 ð 셤 ò a õ 셤 ò polynucleotide 11500

expressed

cancer

Human breast

(first entry)

07-DEC-2001

Human; breast cancer; cell marker; cytostatic;

2001WO-US00798 2000US-0176077

10-JAN-2001;

19-JUL-2001

14-JAN-2000;

WO200151628-A2.

Homo sapiens

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                                                                                                    Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus thost diseases, rheumatoid arthritis, positissis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachesta and autoimmune disease, og. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transpenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology; for diagnostic assays, prognostic assays, prognostic assays, propostic assays, propostice are seculable for monitoring clinical trials. TANGO polypeptides are sustiable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tecgacatgecegeaacgiggacagggteetetgeagetteaagateaatgaeteggtea 796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4417 BP; 1214 A; 1115 C; 994 G; 1094 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 453.2; DB 21;
Pred. No. 6.1e-128;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                of cellular disorders can be treated.
                                                                          209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.18;
90.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                            Claim 1; Fig 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 ggtacaggacagccagcgtcatcattgctttgactgatggagaactccatgaagatctct 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttggtgtgaaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttggtgtgaaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.6%; Score 349; DB 22;
100.0%; Pred. No. 1.3e-96;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 91 A; 78 C; 95 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                 MEDICINE INC
                                                                                                                                                                                                                                                                                        Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE
                                                                                                                                                                             200005-0189167.
200005-0192099.
200005-0193480.
200005-0205230.
200005-020534.
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nes 349; Conserv
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24-MAR-2000;
29-MAR-2000;
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09-JUN-2000;
25-JUL-2000;
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ilarity 100.0%; Pi
Conservative 0;
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2000US-0211315.
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2000US-0192099.
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Best Local Simi
Matches 346;
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                                                                                                          Human breast cancer expressed polynucleotide 590.
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Pred. No. 2.5e-96;
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                                                                                                                                                                                                                                                                                                                                                                                 Steinmann K;
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                                    BP.
                                   AAL08133 standard; cDNA; 355
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24-MAR-2000; 2000US-0192099.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-0205230.
09-JUN-2000; 2000US-0211315.
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(AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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Human breast cancer expressed polynucleotide 18335.
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Pred. No. 1e-95
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  cellular proliferation, cellular differentiation; cellular adhesion, von Willebrand factor-associated disorder; cell trafficking; cancer; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletto associated disease; atelectrasis; pulmonary congestion; ocdems; emphysems; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; brain disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. THE TANGO POLYpeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand
gtgtgaaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatgtgt 180
                                                                                                                                               Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                            ttcccqtqaatqacggctttcaggctctgcaaggcatcatccactcaattttgaagaagt
                                                                                                                            cctgcatcgaaattctagcagctgaaccatccaccatatgtgcaggagagtcatttcaag
                                                                                                                                                                                                         266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
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Matches 627; Conserv
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; schemic heart disease; hydrocephalus; brain hernlation; latrogenic disease; inflammation; meningitis; harbeimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                               1021 ttaagtggaagaggattcatgctgggcagtcggaatggcagtgttctctgcacttacact 1080
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                                                                   atcaatgactcggtcacactcaatgagaagcccttttctgtggaagacacttatttactg
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AAA75157-59 encode human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 26 cellular differentiation and/or modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells chart appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, cand hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral centerial and viral meningitis, Alzheimer's Disease, inflammations, Dactorial and viral meningitis, Alzheimer's Disease, cerebral concers, hydrocephalus and encephalitis, and treat hepatic disorders in the present sequence does not appear in the specification; it was concerned and the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of the conceptual of
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Disclosure; Page -; 175pp; English.
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Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,

2000-579269/54 P-PSDB; AAB18456

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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; ocdema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; isohemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningits; highener's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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                                                                         Disclosure; Page -; 175pp; English.
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58.1%;
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Fraser CC;

Sharp JD,

Holtzman DA,

Barnes TM,

(MILL-) MILLENNIUM PHARM INC

01-MAR-2000; 2000WO-US05226

01-MAR-1999;

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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; von Willebrand factor-associated disorder; cell trafficking; cancer; was associated disease; atelectrasis; pulmonary congestion; oedems; emphysems; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain hernlation; iatrogenic disease; indflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cellular interactions, modulate cellular interactions, modulate the proliferation of disorders, such as cancer modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as isohemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or treat disorders associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                   describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor associated
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                                                                                                                                                                                                                                                                                                                                                                                                                AAA75157-59 encode human TANGO 216 proteins. The specification also
                                                                                                                                                                                                                                                                       Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
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58.1%; Pred. No. 3.5e-94;
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atlectashs; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectashs; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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AAA75160-62 encode murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 262 ellupar beneficially and the tellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Wilebrand factor-associated disorder, requiate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation, and/or function of cells matrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation differentiation, and/or function of bone and cartilage east of sociated and cartilage ells and to treat bone and/or treat diseases or disorder: Any may also be used to treat diseases and sociated and cartilage associated and cartilage associated and cartilage ells and to treat bone and/or treat diseases or disorder: Any may also be used to treat diseases.
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                                                             "TANGO 216"
                                                                                                                                                                                                                                                                                                           Sharp JD,
Location/Qualifiers
149..1612
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Search completed: August 9, 2002, 00:30:32 Job time: 8044 sec

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us-09-970-076-1

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 8, 2002, 23:03:03 Run on:

; Search time 523.51 Seconds
(without alignments)
6309.993 Million cell updates/sec

US-09-970-076-1 1414

Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 ; Gapext 1.0 Scoring table:

2812564 Total number of hits satisfying chosen parameters:

1406282 seqs, 1168085023 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Sequence 176, App	Sequence 231, App	٦	Sequence 17, Appl	1	Sequence 15, Appl	Sequence 23, Appl	19,	Sequence 25, Appl	σ,	Sequence 21, Appl	Ξ	Sequence 11, Appl	Sequence 186, App	Sequence 300, App				"			Sequence 669, App	5, A	6	-
	ΩI		PCT-US02-08253-176	PCT-US02-08253-231	US-10-038-307-1	US-10-038-307-17	US-10-038-307-13	US-10-038-307-15	US-10-038-307-23	US-10-038-307-19	US-10-038-307-25	US-10-038-307-9	US-10-038-307-21	US-09-629-469A-11705	US-10-038-307-11	PCT-US02-08253-186	PCT-US02-08253-300	US-10-047-542-98	US-10-047-542-100	US-10-038-307-3	US-09-918-995-22508	US-09-919-002-11267	US-09-629-469A-3023	US-10-104-047-669	US-10-038-307-5	US-60-373-595-9	US-10-125-540-47
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æ	Query Match		84.4	84.4	74.4	68.1	67.4	67.4	67.3	67.3	67.3	67.2	64.7	62.9	61.4	60.4	60.4	36.8	36.8	32.1	31.3	29.0	26.0	24.5	24.5	24.5	24.1
	Score		1193.8	1193.8	1052.4	962.8	952.4	952.4	951.4	951.4	951	920.8	914.4	890	967.6	853.4	853.4	521	521	453.2	442.2	410	368	346.2	345.8	345.8	341.2
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Sequence 7, Appl1 sequence 19015, A Sequence 13193, A Sequence 12581, A Sequence 1714, Ap Sequence 112, App Sequence 1316, App Sequence 13051, A Sequence 13051, A Sequence 178, App Sequence 178, App Sequence 178, App Sequence 178, App Sequence 178, App Sequence 115, App Sequence 213, App
US-10-038-307-7 US-09-539-800C-19015 US-09-629-4690-4890 US-09-639-331D-12581 US-09-539-331D-12581 US-09-539-331D-27849 PCT-USOZ-13142-7140 US-10-128-714-7140 US-10-128-714-7140 US-10-172-086-112 PCT-USOZ-1918-275 PCT-USOZ-09188-275 PCT-USOZ-09188-275 PCT-USOZ-09137-115 US-10-105-299-377 PCT-USOZ-09135-115 PCT-USOZ-09135-115 PCT-USOZ-09135-115 PCT-USOZ-09135-115 PCT-USOZ-09135-115 PCT-USOZ-09135-115 PCT-USOZ-09135-115
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ALIGNMENTS

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APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Winzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107,00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0 Indels 84.4%; Score 1193.8; DB 1; 99.8%; Pred. No. 9.1e-160; ive 0; Mismatches 2; ; Sequence 176, Application PC/TUS0208253; GENERAL INFORMATION: APPLICANT: Carson-Walter, Eleanor Best Local Similarity 99.8 Matches 1195; Conservative ; ORGANISM: Homo sapiens PCT-US02-08253-176 PCT-US02-08253-176 Query Match TYPE: DNA 121 161 181 241 q ٥y g δ g ŏ g à

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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
                                                                                                                                                                                                                                                                                                                          Sequence 231, Application PC/TUS0208253 GENERAL INFORMATION:
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                                                                               Score 1193.8; DB 1
Pred. No. 9.1e-160;
); Mismatches 2;
CUKKENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
PRIOR PLING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FASTSEQ for Windows Version 4.;
SEQ ID NO 231
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
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CORGANISM: Homo sapiens
US-10-038-307-17
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Pred. No. 7.7e-140;
); Mismatches 1; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFF
APPLICANT: Engin Oxxavnak
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10038307 GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 1053; Conservative 0
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; LOCATION: (213)...(1211)
US-10-038-307-1
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Length 1674;
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DB
        0; Mismatches
Score 962.8;
Pred. No. 3.2
68.18;
99.88;
    Similarity 99.8
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Pred. No. 9.3e-126;
0; Mismatches 6;
                                                                                       and Tango 216
                                                                                                     JMBER: US/10/038,307
2002-06-28
RESULT 5
US-10-038-307-13
Sequence 13, Application US/10038307
Sequence 13, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFF
APPLICANT: Bogin OZKAYNAK
APPLICANT: Judith J. HEALEY
FITLE OF INVENTION: Tango 197
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.06
SEQ ID NO 13
LENGTH 1550
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99.48;
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CORGANISM: Homo sapiens
US-10-038-307-13
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Pred. No. 1.3e-125;
0; Mismatches 1;
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 23
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CORGANISM: Homo sapiens
US-10-038-307-23
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US-10-038-307-23
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Pred. No. 9.3e-126;
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: James B. ROTTMAN
APPLICANT: GIGHT OZKAVNÁK
APPLICANT: GIGHT OZKAVNÁK
TITLE COFINVENTION: Tango 197 and Tango 216 (
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
CURRENT FILING DATE: 2002-06-28
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 15
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ORGANISM: Homo sapiens
US-10-038-307-15
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US-10-038-307-19
NUMBER OF SEQ 3
SOFTWARE: Fast(
SEQ ID NO 19
LENGTH: 1713
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Fheresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Tango 197 and Tango 216
TITLE OF INVENTION: Tango 197
FILE REFRENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
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Score 951.4; DB 7;
Pred. No. 1.3e-125;
0; Mismatches .1;
 67.3%;
99.9%;
         Conservative
     Similarity
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hes 952;
 Query Match
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Pred. No. 1.6e-125;
0; Mismatches 7;
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Graften J. WEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 (FILE REFERRNCE: 7853-253-99)
CURRENT FLILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1650
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ilarity 99.3%;
Conservative
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ORGANISM: Homo sapiens
US-10-038-307-9
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Matches 955; Conserv
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US-10-038-307-9
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Pred. No. 1.5e-125;
0; Mismatches 5; Indels
                                                                                                                      Compositions
                                                                              APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZRAYNAK
APPLICANT: Judith J. HEALEY
TILE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/200-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                               Sequence 25, Application US/10038307 GENERAL INFORMATION:
                                                                                                                                                                                                                                           Query Match 67.3%;
Best Local Similarity 99.5%;
Matches 954; Conservative
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US-10-038-307-25
                                             RESULT 9
US-10-038-307-25
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APPLICANT: ISOGAI, TAKAO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: HAYASHI, KOJI
APPLICANT: SAITO, KAORU
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Endin OZKAYNAK
APPLICANT: Endin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and
TITLE OF INVENTION: Tango 197
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 914.4; DB 7;
Pred. No. 2.2e-120;
0; Mismatches 1;
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al Similarity 97.1%;
952; Conservative
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US-10-038-307-21
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LENGTH: 1047
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SEQ ID NO 2
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Query Match 61.4%;
Best Local Similarity 97.9%;
Matches 879; Conservative (
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; ORGANISM: Homo sapiens
US-10-038-307-11
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US-10-038-307-11
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                                                                      FULL-LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                        62.9%; Score 890; DB 5; 1 99.3%; Pred. No. 5.7e-117;
APPLICANT: YAMAMOTO, JUNICHI
APPLICANT: ISHII, SHIZUKO
APPLICANT: SUGITANA, TOWAYASU
APPLICANT: MAKAMATSU, AI
APPLICANT: NAKAMATSU, AI
APPLICANT: NAGAI, KEIICHI
APPLICANT: OF SUGITANA, TOWAYASU
APPLICANT: NAGAI, KEIICHI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FUL:
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR PRILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PRILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR PRILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 1999-10-18
PRIOR PRILING DATE: 1999-10-18
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Matches 904; Conservative
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SEQ ID NO 11705
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; LOCATION: (380)..(1033)
US-09-629-469A-11705
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Pred. No. 7.9e-114;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10038307;
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa U. O'KEEFE
APPLICANT: Theresa U. O'KEEFE
APPLICANT: Theresa USKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
NUMBER OF SED ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1623
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Pred. No. 7.1e-112;
3; Mismatches 136;
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Best Local Similarity
Matches 935; Conserv
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PCT-US02-08253-186
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                                                                                                                                                                                                                                                                Length 5220;
                           APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bart
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
STOR FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7.1e-112;
0; Mismatches 136;
:r-USO2-08253-300
Sequence 300, Application PC/TUS0208253
GENERAL INFORMATION:
                                                                                                                                                                                                                                                              60.48;
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Best Local Similarity 87.3
Matches 935; Conservative
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PCT-US02-08253-300
                                                                                                                                                                                   SEQ ID NO 300
LENGTH: 5220
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Search completed: August 9, 2002, 02:02:44 Job time: 10781 sec

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets o results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- nucleic search, using sw model OM nucleic

8, 2002, 22:18:18 August Run on:

; Search time 4997.37 Seconds
(without alignments)
6121.569 Million cell updates/sec

US-09-970-076-1 Perfect score:

Title:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

43959072 Total number of hits satisfying chosen parameters:

21979536 segs, 10817449327 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2_6/ptodata/2/pna/US085_COMB.seq: /cgn2_6/ptodata/2/pna/US086_COMB.seq: /cgn2_6/ptodata/2/pna/US086_COMB.seq: /cgn2_6/ptodata/2/pna/US089_COMB.seq: /cgn2_6/ptodata/2/pna/US089_COMB.seq: /cgn2_6/ptodata/2/pna/US092_COMB.seq: /cgn2_6/ptodata/2/pna/US092_COMB.seq: /cgn2_6/ptodata/2/pna/US092_COMB.seq: /cgn2_6/ptodata/2/pna/US093_COMB.seq: /cgn2_6/ptodata/2/pna/US093_COMB.seq: /cgn2_6/ptodata/2/pna/US093_COMB.seq: /cgn2_6/ptodata/2/pna/US093_COMB.seq: /cgn2_6/ptodata/2/pna/US093_COMB.seq: /cgn2_6/ptodata/2/pna/US095_COMB.seq: /cgn2_6/ptodata/2/pna/US095_COMB.seq: 12.6/ptcdata///pna/US0950__COMB.seq: 12.6/ptcdata///pna/US0950__COMB.seq: 12.6/ptcdata///pna/US096a_COMB.seq: 12.6/ptcdata///pna/US096b_COMB.seq: 12.6/ptcdata///pna/US096c_COMB.seq: 12.6/ptcdata///pna/US096c_COMB.seq: 12.6/ptcdata///pna/US097a_COMB.seq: 12.6/ptcdata///pna/US097a_COMB.seq: 12.6/ptcdata//pna/US097a_COMB.seq: 12.6/ptcdata//pna/US097a_COMB.seq: 12.6/ptcdata//pna/US098a_COMB.seq: 12.6/ptcdata//pna/US098a_COMB.seq: 12.6/ptcdata//pna/US098a_COMB.seq: 12.6/ptcdata//pna/US098a_COMB.seq: 12.6/ptcdata//pna/US099a_COMB.seq: 12.6/ptcdata//pna/US099a_COMB.seq: 12.6/ptcdata//pna/US099a_COMB.seq: 12.6/ptcdata///pna/US099a_COMB.seq: 12.6/ptcdata///pna/US099a_COMB.seq: 12.6/ptcdata///pna/US099a_COMB.seq: 12.6/ptcdata///pna/US099a_COMB.seq: 12.6/ptcdata///pna/US099a_COMB.seq: 13.6/ptcdata///pna/US099a_COMB.seq: 14.6/ptcdata///pna/US099a_COMB.seq: 15.6/ptcdata///pna/US099a_COMB.seq: 16.6/ptcdata///pna/US099a_COMB.seq: 17.6/ptcdata///pna/US099a_COMB.seq: 17.6/ptcdata///pna/US099a_COMB.seq: 17.6/ptcdata///pna/US099a_COMB.seq: Pending_Patents_NA_Main:*

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3: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/USO81_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/USO81_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/USO83_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/USO83_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/USO83_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/USO83_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/USO83_COMB.seq:*
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7: /cgn2_6/ptodata/2/pna/USO83_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/USO83_COMB.seq:* 6/ptodata/2/pna/US095C_COMB.seg:* 'pna/US101_COMB.seq:* _6/ptodata/2/pna/US6001_COMB.seq: _6/ptodata/2/pna/US6002_COMB.seq:

/cgn2_6/ptodata/2/pna/US6003_coMB.seq:* /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*

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	gn2_6/ptodata/2/pna/U	75
	todata/2/pna/US6035_CO	74
	gn2_6/ptodata/2/pna/US6034_C	73
	gn2_6/ptodata/2/pna/US6033_COMB.s	72
	n2_6/ptodata/2/pna/US6032_C	7.1
	n2_6/ptodata/2/pna/US6031_C	70
	n2_6/ptodata/2/pna/US6030_C	69
	gn2_6/ptodata/2/pna/US6029_CO	
	n2_6/ptodata/2/pna/US6028_C	67
	gn2_6/ptodata/2/pna/US6027_C	99
	gn2_6/ptodata/2/pna/US6026_C	65
	gn2_6/ptodata/2/pna/US6025_C	
	n2_6/ptodata/2/pna/US6024_C	63
	n2_6/ptodata/2/pna/US6023_	62
	gn2_6/ptodata/2/pna/US6022_COMB.se	
	qn2_6/ptodata/2/pna/US6021_COMB.	
	gn2_6/ptodata/2/pna/US6020_COMB.	
	qn2_6/ptodata/2/pna/US6019_COMB.	58
	qn2_6/ptodata/2/pna/US6018_COMB.	57
	qn2_6/ptodata/2/pna/US6017_COMB.se	26
	gn2_6/ptodata/2/pna/US6016_	55
	n2_6/ptodata/2/pna/US6015_COMB.	54
	qn2_6/ptodata/2/pna/US6014_COMB.se	53
	qn2_6/ptodata/2/pna/US6013_	52
	gn2_6/ptodata/2/pna/US6012_COMB.s	51
	n2_6/ptodata/2/pna/US6011_COMB.s	20
	qn2_6/ptodata/2/pna/US6010_COMB.se	49
	n2_6/ptodata/2/pna/US6009_C	48
	n2_6/ptodata/2/pna/US6008_COMB.s	47
	qn2_6/ptodata/2/pna/US6007_C	46
	qn2_6/ptodata/2/pna/US6006_COMB.s	45
	n2_6/ptodata/2/pna/US6005_C	44

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli Sequence 1222, Ap	176, 4	231,	ď,	Sequence 14, Appl	Seguence 45, Appl	Sequence 7, Appli	۵,	æ	Sequence 8, Appli	Sequence 8, Appli	Sequence 11, Appl				204,	966	204,	68,	866	Sequence 998, App	7727,	7637,			Sequence 5593, Ap	Sequence 7873, Ap	7727,		Sequence 1757, Ap
di di	US-09-970-076-1	-17	7	US-09-970-076-5	7	ı.	•	PCT-US99-31025-8		US-09-471-179-8	US-09-599-596-8	$\overline{}$	-09-644-871-9	US-09-710-281-4357	-329-548A-	US-09-419-553-204	US-09-516-448-998	-770-155-2	US-09-780-183-68	-833-381-9	-833	US-09-371-168-7727	US-09-644-868-7637	US-09-644-871-7309	-649-163-	US-09-652-121-5593	-652-127-7	-801-833-77	-09-668-337-18	US-09-625-102-1757
DB	36	34	34	36	щ	Н	36	7	16	18	22	30	25	28	17	18	19	30	30	32	32	17	25	25	25	25	25	31	56	24
Query Match Length	1414	5540	5540	5540	2447	2086	2112	2272	2272	2272	2272	2272	2374	2374	2459	2459	2459	2459	2459	2459	2459	2401	2401	2401	2401	2401	2401	2401	2485	2397
Query Match	100.0	84.4	84.4	84.4	84.4	84.3	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.3	4.	4	74.3	4	74.3	4.	72.5	68.1
Score	1414	1193.8	1193.8	1193.8	1193.6	1192.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1050.8	1050.8	1050.8	1050.8	1050.8		1050.8	•	963
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9.4 67.1 999 1 PCT-US99-31025-10 Sequence 10.9.4 67.1 999 10 CG-US-23-564-610 Sequence 10.9.4 67.1 999 18 US-09-471-179-10 Sequence 10.9.4 67.1 999 18 US-09-471-175-197 Sequence 10.9.8 64.1 1609 18 US-09-488-7258-3907 Sequence 10.9.9 14 US-09-918-715-18 Sequence 10.9.9 14.0 US-09-918-715-18 Sequence 10.9.9 14.0 US-09-918-715-18 Sequence 10.9.9 14.0 US-09-918-715-18 Sequence 10.9 US-09-918-	, 0 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 176, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: 06/222,599
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
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SPIOR APPLICATION NUMBER: 60/224,360
SPIOR APPLICATION NUMBER: 60/224,360
SPIOR FILING DATE: 2000-04-11
SPIOR APPLICATION NUMBER: 60/282,850
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SPIOR APPLICATION NUMBER: 60/282,850
SPIOR FILING DATE: 2000-04-11
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; ORGANISM: Homo sapiens
US-09-918-715-176
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                                                                        APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Tolontified Thereby
TITLE OF INVENTION: Tolontified Thereby
FILE REFERENCE: Gx-0015 P
CURRENT APPLICATION NUMBER: US/60/213,359
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 7924
SOFTWARE: PERL Program
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Pred. No. 5.6e-131;
0; Mismatches 2; Indels
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COTHER INFORMATION: Incyte ID No: 243308.2
US-60-213-359-1222
                              Sequence 1222, Application US/60213359
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
                                                                                                                                                                                                                                                                                                                                                                                      84.48;
99.88;
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Best Local Similarity 99.8
Matches 1195; Conservative
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                US-60-213-359-1222
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Sequence 231, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107 00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR PAPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-04-11
PRIOR PILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
SUMBER OF SEQ ID NOS: 358
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 231
LENGTH: 5540 Indels 34; Score 1193.8; DB 3-Pred. No. 5.1e-131; 0; Mismatches 2; 84.4%; .larity 99.8%; Conservative sapiens Similarity ; ORGANISM: HOMO US-09-918-715-231 Best Local Sim Matches 1195; DNA Query Match 461 521 481 541 421 281 341 361 121 161 181 221 241 301 401

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Pred. No. 5.1e-131;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                             APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296,97745
CURRENT APPLICATION NUMBER: 08/09/970,076
CURRENT APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09970076 GENERAL INFORMATION:
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99.8%;
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Best Local Similarity 99.8
Matches 1195; Conservative
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; LOCATION: (144)..(1835)
US-09-970-076-5
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 5 US-09-970-076-5

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; Sequence 45, Application Sciences, Inc.
; Sequence 45, Application:
    APPLICANT: Human Genome Sciences, Inc.
    TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PS708PCT
; CURRENT APPLICATION NUMBER: PCT/US00/30045
; CURRENT FILING DATE: 2000-11-01
; PRIOR FILING DATE: 1999-11-05
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEC ID NOS: 201
; SEC ID NOS: 201
; SEC ID NOS: 201
; SEC ID NOS: 201
; SEC ID NOS: 204
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LOCATION: (2070)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (2075)
OTHER INFORMATION: n
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INFORMATION:
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OTHER INFORMATION:
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LOCATION: (2083)
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LOCATION: (2079
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OTHER INFO
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APPLICATE: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT:
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR PLING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 201
SOFTWARE: PATENTIN VOI: 2.0
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Pred. No. 5.9e-131;
); Mismatches 4;
                                                                             Sequence 14, Application PC/TUS0030045 GENERAL INFORMATION:
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99.78;
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PCT-US00-30045-14
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Matches 1196;
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                                                                                                                                                                         APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 960296, 97745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 7
                                                                                                                                                          Sequence 7, Application US/09970076 GENERAL INFORMATION:
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; LOCATION: (113)..(1111)
US-09-970-076-7
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ORGANISM: HOMO
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                                   DB 1;
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Pred. No. 8.4e-131
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GENERAL INFORMATION:
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99.98;
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LOCATION: (213)...(1211)
-US99-31025-8
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1053; Conserv
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PCT-US99-31025-8
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                           NUCLEIC ACIDS
                                                                                                                     Score 1052.4; DB 16;
Pred. No. 2e-114;
0; Mismatches 1; Ir
   US-09-223-546-8

Sequence 8, Application US/09223546

GENERAL INFORMATION:
FITLE OF INVENTION: SECRETED PROTEINS AND NUFICE REFERENCE: 09404/066001

CURRENT APPLICATION NUMBER: US/09/223,546

CURRENT FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                     74.48;
99.98;
                                                                                                                           Best Local Similarity 99.9
Matches 1053; Conservative
                                                                                            , LOCATION: (213)...(1211)
US-09-223-546-8
                                                            SEQ ID NO 8
LENGTH: 2272
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                         NAME/KEY: CDS
LOCATION: (21)
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US-09-471-179-8
Sequence 8, Application US/09471179
Sequence 8, Application US/09471179
GENERAL INFORMATION:
APPLICANT: HOITZMAN DOUGLAS
TITLE OF INVENTION: SECRETED PROTEINS AND NUC
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 8
SEQ ID NO 8
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Best Local Similarity 99.9%;
Matches 1053; Conservative (
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; LOCATION: (213)...(1211)
US-09-471-179-8
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8-965-665-80

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                                                                     NUCLEIC ACIDS ENCODING
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (213)...(1211)
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DB 22;
Score 1052.4; DB 22
Pred. No. 2e-114;
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                                Score 1052.4; DB
Pred. No. 2e-114;
0; Mismatches
                                  74.48;
99.98;
                                  Query Match 74.4
Best Local Similarity 99.9
Matches 1053; Conservative
     ; NAME/KEY: CDS
; LOCATION: (213)...(1211)
US-09-796-753-11
FEATURE:
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                                                  Sequence 11, Application US/09796753 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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LENGTH: 2272
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ORGANISM: Homo sapiens
US-09-710-281-4357
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Matches 1053; Conserv
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; GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1167-001
CURRENT APPLICATION NUMBER: 05/09/644,871
CURRENT FILING DATE: 2000-08-28
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9739
SOFTWARE: FEASTER FOR Windows Version 4.0
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Pred. No. 2e-114;
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US-09-644-871-9264
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LENGTH: 2374
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US-09-710-281-4357
US-09-710-281-4357
Sequence 4557, Application US/09710281
Sequence 4557, Application US/09710281
Sequence 4557, Application US/09710281
Sequence 4557, Application US/09710281
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
TITLE COF INVENTION: THEREFOR
CURRENT APPLICATION UNDERS: US/09/710,281
CURRENT FILING DATE: 2000-11-10
SPRIOR PILING DATE: 1999-11-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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Q96ft5 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 GGGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; "Identification of the Cellular Receptor for Anthrax Toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Sukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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 09p218 09bqu7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8A87B13FFA7D8753 CRC64;
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Last annotation update)
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O
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100.0%; Pred. No. 4.6e-127;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AA
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Q9P218
Q9BQU7
Q63870
Q21281
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096815
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0971C5
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EMBL; AF421380; AAL26496.1;
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Best Local Similarity 100.(
Matches 295; Conservative
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09bpg8 halocynthia
004588 eimeria max
043981 eimeria ten
070350 mus musculu
09u819 neospora ca
043853 homo sapien
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Q99117 mus musculu
Q9ual3 caenorhabdi
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497.015 Million cell updates/sec
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09es77 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96p02 homo sapien
Q96nc7 homo sapien
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096ec6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                          9, 2002, 10:46:19; Search time 102.68 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                      ....GLSFISSSVIITTTHCSDGS
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                                                                                    562222 seqs, 172994929 residues
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1 GOGGRREDGGPACYGGFDLY....
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                                                                - protein search, using sw model
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Maximum DB seq length: 200000000
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DREQIRQGLEELOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                              DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                                                                                                                       Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallatin W.M., VanderVieren M., Kilgannon P.D., Dietsch G Gallatin W.M., VanderVieren M., Kilgannon P.D., Dietsch G Gallatin W.M., VanderVieren M., Kilgannon P.D., Dietsch G Gallatin W.M., VanderVieren M., VanderVieren J., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AR021334, AR721241.1; -. HSSP: P11215; 1A8X. InterPro; IPR000413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2258491A984A705E CRC64;
                                                                                                                                                                                                                                                                                                                 Indels
                                   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC012475; AAH12475.1; -.
                                                                                                                                                                       SEQUENCE 97 AA; 10453 MW; 14F475F0B170E71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA D INTEGRIN
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                                                                                                                                                                                                                                                               Score 388; DB 4; L
Pred, No. 9.2e-27;
D: Mismatches 4;
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[1]
EGUGENCE FROM N.A.
TISSUB-BREAST, AND MAMMARY ADENOCARCINOMA;
Strausberg. R.; AND MAMMARY ADENOTATION OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF THE ENDINGERIES OF
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Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 VSMNDGLSFISSSVIITTHCS 292
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nilarity 95.1%;
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STRAIN=SPRAGUE-DAWLEY;
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Matches 63; Conserv
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nes 78; Conserv
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                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 LRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Ninomiya K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamiazaki M., Sugiyama T., Irie R., Otsuta N., Sato H., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Kawai Hio Y., Sato H., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Matsuo K., Nakamura Y., Sekine M., Kiuchi H., Murakawa K., Yamashita H., Marakawa K., Yamashita H., Murakawa K., Yamashi B., Sauzuk Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (COT-2001) to the EMBL/GenBank/DDBJ databases.

ENBL, AKO55636; BAB703761; --
SEQUENCE 245 AA; 26111 MW; BIAE6EB0A2EBEE06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        096EC6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0NKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: :|:: | : || ||: :||!|||||: |
179 TYTVNETYTTSVKPVSVQLNSMLCPAPILNKAG------EWGLTVTQAGVKWHDLTH
     207 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                        37.4%; Score 574; DB 4; Length 245;
49.2%; Pred. No. 1.4e-42;
tive 45; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                245 AA
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01-DEC-2001 (TrEMBLrel. 19, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annoti
CDNA FLJ31074 FIS, CLONE HSYRA2001476.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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230 CTFG 233
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MEDLINE-93149203; PubMed-8426611;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
Sequence of a major Eineria maxima antigen homologous to the Eineria tenella microneme protein Etp100.";
Mol. Blochem. Parasitol. 57:171-174(1993).
EMBL; M99058; AAA29076.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR0002035; vWFA.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HOUGHTON;
MEDLINE=92131064; PubMed=1775171;
Tomley F.M., Clarke L.E., Kawazoe U., Dijkema R., Kok J.J.;
Tomley F.M., Clarke L.E., Kawazoe U., Dijkema R., Kok J.J.;
"Sequence of the gene encoding an immunodominant microneme protein of Elmeria tenella.";
Mol. Biochem. Parasitol. 49:277-288(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 SDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 A-----SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 CTRLLDVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 ELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Elmeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 TEDREQIRQCLEELQKVLP - GGDTYMHEGFERASEQIYYENRQGYR - TASVIIALTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.0%; Score 139; DB 5; Length 72.
26.6%; Pred. No. 0.0012;
tive 40; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC2A0E7A346A7E9E CRC64;
                                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) MAJOR ANTICE HOMOLOGOUS SEQUENCE (EMP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 -VNDGFQALQGIIHSILKKSCIEI----LAAEPSTI--CAGE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 YLQSNWGGVSSQINGIIKAACKDLAKDAVCSEWSEYGPCEGE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MICRONEME PROTEIN ETMIC-1 PRECURSOR.
                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00453; VWPADOMAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 5.
PROSITE: PS50234; VWFA; 1.
SEQUENCE 724 AA; 75808 MW;
                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
    PRELIMINARY;
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Best Local Similarity
Matches 59; Conserv
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NCBI_TaxID=5802;
                                                                                                                                                                              NCBI_TaxID=5804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elmeria tenella
                                                                                                                       Eimeria maxima.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDLGAIVYCVGVKDFNETQLARIA---DSKDHVFPVNDGFQALQGIIHSILKKSCIEILA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGRREDGG-----PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::|
DRI---QLQGYTTYTGRALQKVIRDFDDAYIGNKQYLLLLTDGQAKDNKLILP--NANRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miyazawa S., Azumi K., Nonaka M.; "Cloning and characterization of integrin alpha subunits from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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CHAIN 31 1332 INTEGRIN ALPHA HRI.
SEQUENCE 1332 AA; 145852 MW; 0D9108D2805CFFAE CRC64;
                                                                     323 LRSIQRQLQEK----IFAIEGTQSRSSSSFQHEMSQEGFSSALTSD 364
                                       182 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                        Halocynthia roretzi (Sea squirt).
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIN ALPHA HRI PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%; Score 153.5; DB 5; 24.1%; Pred. No. 0.00015; ative 42; Mismatches 81;
                                                                                                                                                                                  PRT; 1332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            solitary ascidian, Halocynthia roretzi.";
J. Immunol. 166:1710-1715(2001).
EMBL; AB040261; BAB21479.1; -.
HSSP; PI115; 1A8X.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-HEMOCYTE;
MEDLINE-21103187; PubMed-11160215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam, PF01839; FG-GAP; 5.
Pfam, PF00357; Integrin_A; 1.
Pfam; PF00302; vwa; 11.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SWART; SW00191; Int_alpha; 5.
SNART; SW00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGKSAKTAG--YEMHFGENGF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEPSTICAGESFQVVVRGNGF 220
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Best Local Similarity 24.1%
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                                                                                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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765 AA.
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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00032; CCP: 2.
SMART; SM00030; TYP_SPC; 1.
SMART; SM00327; VWA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 MND-----GLSFISSSVII 286
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; "Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 TEDREQIRQGLEELQKVLPG------GDTYMHEGFERASEQIYYENRQGYR-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 CTSLLDVMLVVDESGSIGTSNFRKVR@FIEDFVNSMPISPEDVRVGLITFAT----- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                       A Relleher W., Tomley F.W.;

A Relleher W., Tomley F.W.;

Translent expression of beta-galactosidase in differentiating sporozoites of Eimeria tendella.";

L Mol. Biochem. Parasitol. 97:21-31(1998).

EMBL; AF032905; AAD03300.1; -. 37:21-31(1998).

R HSSP: P17301. 1A0X.

R InterPro; IPR002035; WFA.

R InterPro; IPR002035; WFA.

R Pfam; PF00090; tsp_1; 6.

R PRINTS; PR00453; WFADOMAIN.

R SMART; SM00209; TSP1; 6.

SMART; SM00209; TSP1; 6.

R PROSITE; PS50034; VWFA. 1.

R PROSITE; PS50034; VWFA. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas Hood L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
MICRONEME PROTEIN ETMIC-1.
15B8F3C190B70F73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 P-----VNDGFQALQGIIHSILKKSCIEILAAEPSTI--CAGE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 PRYLQSNWSNVTQQVNGIIKAACKDLAKDAVCSEWSEYGPCVGE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

8.8%; Score 134.5; DB 5;
Best Local Similarity 24.6%; Pred. No. 0.0029;
Matches 55; Conservative 40; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 291-760 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN 37 712 M. SEQUENCE 712 AA; 74777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                  FROM N.A.
                                          STRAIN=HOUGHTON;
MEDLINE=99094493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   070350;
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Neospora caninum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----KD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 GHLNLYLLLDASQSVTEKDFIFKKSAELMVERIFSFEVNVSVALITFASQPKTIMSILS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-------NRQGYRTAS- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLRMS--FIVFSTRGTTLMKLTE 71
Strausberg R.;
L. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
L. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY:
R. EMBL; AR109906; AAC84162.1; -.
R. EMBL; AR109806; AAC84162.1; -.
R. EMBL; AR110866; AA.11086.1; -.
R. EMBL; BC011086; AAH11086.1; -.
R. MGD; MGITS18226. C2.
R. MGD; MGITS18226. C3.
R. InterPro; IPR001314; Chymotrypsin.
R. InterPro; IPR00134; Chymotrypsin.
R. InterPro; IPR001254; Trypsin.
R. Pfam; PF00089; Luxpsin; 2.
R. Pfam; PF00089; Luxpsin; 2.
R. Pfam; PF00089; Luxpsin; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.7%; Score 134; DB 11; Length 760; Best Local Similarity 23.5%; Pred. No. 0.0035; Matches 75; Conservative 55; Mismatches 115; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00327; VWA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 2.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_ESR; UNKNOWN_1.
PROSITE; PS50234; VWRA; 2.
PROSITE; Serine protease.
SEQUENCE 760 AA; 84741 MW; 91C896A3EDC7D448 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
THROWBOSPONDIN-RELATED ADHESIVE PROTEIN HOMOLOG.
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16;

14;

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128 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 TILMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 DREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 127
                                                                                                                                120 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVND 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE 71
                                                                                                               13 CYGGFDL---YFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  29;
                                                      DB 4; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 660;
                                                      Query Match 8.6%; Score 131.5; DB 4; Length Best Local Similarity 29.6%; Pred. No. 0.0035; Matches 61; Conservative 39; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72523 MW; 3E3A10A285ECAA51 CRC64;
             56727 MW; 9B6972F44A1BD88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DD334P15.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 131; DB 4;
29.8%; Pred. No. 0.0054;
tive 38; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                           660 AA
                                                                                                                                                                                                                                                                                         178 GFQALQGIIHSILKKSCIEI---LAA 200
                                                                                                                                                                                                                                                                                                                  303 -FDAFORISFELTQSICLRIEQELAA 327
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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517 5
517 AA;
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SEQUENCE FROM N.A.
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SEGUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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م
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                                                                                                                                                                                                                                                                                                                                                                                                        66 LMKL----TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY-YENRQGYRTASVII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   128 HWSLRANNASDKETAMO--DVLTIPYHGGTTNTAAGLQTCNQMLFDYPREERQTVPKLVI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF-NETQLARIADSKDHVFP----V 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wessel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.;
"Type XII collagen contributes to diversities in human corneal and
limbal extracellular matrices.";
Invest. Ophthalmol. Vis. Sci. 38:2408-2422(1997).
EMB.; 068199; AAC01506.1; -.
HSSP: P17301; 1AOX.
InterPro: IPR003961; FN_III.
InterPro: IPR003961; VWFA.
Pfam; PF00041; fn3; 3.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                              13 CYGGFDLYFILDKSGSVLH-HWNEIYYFVEQLAHKFIS-----PQLRMSFIVFSTRGTT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN 1998 (TrEMBLrel. 06, Created)
01-JUN 1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TYPE XII COLLAGEN (FRGMENT).
TYPE XII COLLAGEN (FRGMENT).
FUN Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          Lovett J.L., Howe D.K., Sibley L.D.; Molecular characterization of a thrombospondin-related anonymous
                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                      Length 765;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                              765 AA; 82880 MW; 9727838CC1FE8CD4 CRC64;
                                                                                                                                                                                                                                                                                      Query Match 8.6%; Score 132.5; DB 5; Best Local Similarity 25.1%; Pred. No. 0.0048; Matches 50; Conservative 35; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 AA
                                     protein homologue in Neospora caninum.";
Nol. B.ochem. Parasitol. 107:33-43(2000).
EMBL, AFOGLI273, AAFOLIS6.1;
InterPro; IPR001969; ASP_protease.
InterPro; IPR000884; TSPI.
InterPro; IPR00055; WWFA.
Pfam; PF00090; tsp_1; 6.
Pfam; PF00090; vwa; 1.
                                                                                                                                                  PRINTS: PRO0453: VWFADOMAIN.
SMART: SM00209; TSP1: 6.
SMART: SM00327; VWA; 1.
PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
PROSITE: PS50092; TSP1: 6.
PROSITE: PS50234; VWFR; 1.
SEQUENCE 765 AA; 82880 MW; 9727838CC1F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
MEDLINE-20183852; PubMed-10717300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-CORNEA;
MEDLINE-98003048; Pubmed-9344363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 NDGFQALQGIIHSILKKSC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 QTEWSQLLPSISPILKEVC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0453; VAFADOMAIN.
SMART; SM00060; FN3; 3.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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043853
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-3 PRECURSOR (K08E5.3 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
                                                                                                                                   8.3%; Score 128; DB 11; Length 221;
ilarity 44.2%; Pred. No. 0.0022;
Conservative 12; Mismatches 17; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                           243 EKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDG
                                                                                                                                                                                                             SIRANNEY, VOGEL B., Hedgecock E.; "un 2., Vogel B., Hedgecock E.; "mu 2., RNA Splicing Pattern Revealed."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kersnaw J.K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                    Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003908; AAH03908.1; -.
Hypothetical protein.
1 1
SEQUENCE 221 AA; 24505 MW; 31AB702E42E9CEB3 CRC64;
                                                                                                                                                                                                                                                                                            PRT; 3767 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000152; Asx_hydroxyl. Interpro; IPR001762; Disintegrin. Interpro; IPR001881; EGF-11ke. Interpro; IPR001881; EGF_Ca. Interpro; IPR001881; EGF_Ca. Interpro; IPR001882; EA. Interpro; IPR000082; SEA. Interpro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating blology.";
Science 282:2012-2018(1998).
EMBL; AF139060; AAD29428.1;
EMBL; 230974; CAA83226.2; JOINED.
HSSP; P01130; 1LDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00057; Idl_recept_a; 4. Pfam; PF01390; SEA; 2. Pfam; PF00092; vwa; I. PRINTS; PR00289; DISINTEGRIN. PRINTS; PR00289; LDLRECEPTOR. PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF_CA; 1.
EGF_like; 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00181; EGF; 51.
SMART; SM00179; EGF_CA; 1
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00008; EGF; 33.
                                                                                                                                                      Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00179;
SM00001;
SM00192;
SM00200;
                                                                                                                                                                                                                                                                                                                                                                                           MUA-3 OR K08E5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                            Q9UA13; Q21340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-N2;
                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT)
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                 Q9UA13
                                                                                                                                                                                                                                                                       RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYR- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 THETENDEKRNPSPKLLVRPIRQLL------GRTHTATGIRKVVRELFH-SKŞGARE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 NALKILVVITDGEKFGDPLGYEDDIRFADRK---GVIRYVIGVGDAFNSWKSREELNTIA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISP---QLRMSFIVFSTRGTTLMKLTED-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 DSK--DHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 SKPCGDHVFQVNN-FEAVKTIQNQLQEKT----FAIEGTQTGSTSSFECEMSQEGFSAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                        Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%; Score 130.5; DB 6; Length 920; 26.4%; Pred. No. 0.0093; Live 41; Mismatches 72; Indels 63
                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMITTED (NOV-1995) to the EMBL/GenBank/DDBJ databases.
SUBMITTED (NOV-1995) to the EMBL/GenBank/DDBJ databases.
SUBMITTED (NOV-1995) to the EMBL/GenBank/DDBJ databases.
INTECFP: 1125, 1A8X.
INTECFP: 1PR002013; VWFA.
Pfam; PF001893; FG-GAPP; 4.
Pfam; PF001892; VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       920
102440 MW; E96CC51E350DD5AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                 920 AA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-JUN-2001 (TrEMBLrel. 19, Last annotatic
HYPOTHETICAL 24.5 KDA. PROTEIN (FRAGMENT)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                            Created)
                                                                                                                  PRT;
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PRINTS; PRO1453; VWFADOMAIN.
SMART; SM00191; Int_alpha: 4.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
NON_TER 920
SEQUENCE 920 AA; 102440 MW;
                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19, CD11B (FRAGMENT).
                                               638 SFELTQSICLRIEQELAA 655
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Best Local Similarity 26.4%
Watches 63; Conservative
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                       186 IHSILKKSCIEI---LAA
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Q28984;
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                                                                                                                                                                                                                                                                                                                          1318 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN 1364
                                                                                                                                               POTENTIAL.
TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-
                                                                                                                                                                                                                                                                                                                                                                                                                           --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 15, Last annotation update)
10-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1NTEGRIN BETA 2 ALPHA SUBUNIT.
1RATURIN norvedicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                              66; Gaps
                                                                                                                                                                                                                                                                                                                                                                  45 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH- 95
                                                                                                                                                                                                                                                                                                          13 CYGGF------WNEIYYFVEQLA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium-binding; EGF-like domain; Glycoprotein; Receptor; Repeat; Signal. 1 24 DOMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 203
                                                                                                                                                                                                                                                ; Score 128; DB 5; Length 3767;
; Pred. No. 0.11;
31; Mismatches 75; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fathallah D.M. Sr., Zerria K. Jr.;
"Cloning of the rat CDIIb cDNA sequence.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF268593; AAF61280.1;
                                                                                                                                                                                       3767 3767
3767 AA; 417284 MW; BDA3AE5EA50AEBBE CRC64;
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            PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_32.
PROSITE; PS01186; BGF_1; UNKNOWN_1.
PROSITE; PS01186; BGF_2; 6.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS50068; LDLRA_2; 2.
PROSITE; PS50024; SEA; 4.
PROSITE; PS50234; VWFA; 2.
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InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002043; WFA.
Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
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PROSITE; PS50234; VWFA; 1.
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Best Local Similarity 27.1%;
Matches 64; Conservative 31
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PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
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SM00327; VWA; 1.
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SEQUENCE FROM N.A.
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SEQUENCE
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Length 1151;

8.0%; Score 123; DB 11; 23.9%; Pred. No. 0.058;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                  124 DGELHEDLFFYSEREANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFPVN 176
                                                                                                                                                                                                                                                                                                                               177 DGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKIN 236
                                                                           ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 123
Gaps
                                              18 DLYFILDKSGSVLHHWNEIXYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 72
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ITSN------GPLGSVGSFDWAGGAFLYPSKDKASFINITRI 395
                                                                                                                                                                                                                                                                                                                                                                                                                         237 DSVTLNEKPFSVEDTYLLCPAPILKEVG----MKAALQVSMNDGLSFISSSVI 285
                                                                                                                                                                                                                                                                                                                                                            46; Mismatches 105; Indels
  Conservative
  70;
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Search completed: August 9, 2002, 10:46:21 Job time: 844 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bishop, David F.
APPLICANT: Icannou, Yiannis A.
APPLICANT: Wang, Anne M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGALACTOSAMINIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION UMBER: US/07/602,608
FILING DATE: 24-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 51.6; DB 1;
                          US-08-665-966-9
US-09-041-780-9
US-09-182-816-22
US-09-182-816-24
US-09-182-816-24
US-09-471-528-22
US-09-471-528-22
US-09-634-530-22
US-08-634-530-24
US-08-933-823-7
US-08-933-823-7
US-08-993-228-3
US-08-993-228-3
US-08-993-228-3
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOMETHARE: Patentin Release #1 n ...
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-(
TELECOMMUNICATION INFORMATION:
TELEFRONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/07602608
Patent No. 5382524
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APPLICANT: Desnick, Robert J.
APPLICANT: Bishop, David F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAHITA A
                1454
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435
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STATE: New York
COUNTRY: U.S.A.
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STREET: 11
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US-07-602-608-1
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US-07-602-608-1
Query Match
(without alignments)
3166.719 Million cell updates/sec
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Sequence 3, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 15, Appl
Sequence 75, Appl
Sequence 17, Appl
Sequence 17, Appl
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Sequence 8, Appl
Sequence 37, Appl
Sequence 37, Appl
Patent No. 5196333
Sequence 10, Appl
Sequence 16, Appl
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Sequence 6, Appli
Sequence 595, App
Sequence 1, Appli
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                                  Compugen Ltd.
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US-09-195-666A-16
US-09-309-592-10
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                  Run on:
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RESULT 3
US-08-631-097-8
US-08-631-097-8
Sequence 8, Application US/08631097
Sequence 8, Application US/08631097
Sequence 8, Application US/08631097
Sequence 8, Application US/08631097
Sequence 8, Application US/08631097
TITLE OF INVENTION: Tumor Suppressor Genes, TITLE OF INVENTION: Proten Encloded Thereby, and Use of Said Genes and Protein NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
2025 CACIGGGAGTGAGGGTCACAAAGGAGACCTTGGCTCCCTCAGGTCACCAATAAACCTGTT 2084
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers, P.C.
1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wigman, Cohen, Leitner, & STREET: 900 17th Street, N.W., Suite CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,097
FILING DATE: 12-Apr-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11598
FILING DATE: 12-Oct-94
FILING DATE: 12-Oct-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: not applicable INDIVIDUAL ISOLATE: not applicable DEVELOPMENTAL STAGE: not applicable HAPLOTYPE: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATOMACTIC CONENT, Herbert
REGISTRATION NUMBER: 25,109
REGISTRATION NUMBER: 0744.057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)463-7700
TELEFAX: (202)463-7700
TELEFAX: (202)463-76915
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3829 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANELLE: not applicable
IMMEDIATE SOURCE:
ILIBRARY: not applicable
CLONE: not applicable
CLONE: not applicable
CHROMOSOME/SEGMENT: not applicable
MAP POSITION: not applicable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: Dlood
CELL TYPE: leucocyte
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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ORGANISM: homo
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                                                                                   2025 CACTGGGAGTGAGGGCACAAAAGGAGACCTTGGCTCCCTCAGGTCACCAATAAACCTGTT 2084
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Pred. No. 0.00038; J. Mismatches 49; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Deshick, Robert J.
APPLICANT: Bishop, David F.
APPLICANT: Icannou, Yiannis A.
APPLICANT: Wang, Anne M.
APPLICANT: Wang, Anne M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGALACTOSAMINIDASE
NUMBER OF SEQUENCES: 24
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUTY: New YOLK

COUNTY: New YOLK

COUNTY: U.S.A.

ZIPE: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,578
FILING DATE: 17-UN-1994
CLASSIFICATION NUMBER: US 07/602,608
FILING DATE: 24-OCT-1990
ATTONREY/AGNET INFORMATION:
APPLICATION NUMBER: 30,742
REGISTRATION NUMBER: 6923-008
FELEPRACE/POCKET UNMBER: 6923-008
TELEFRA: (212) 790-9090
TELEFRA: (212) 790-9090
TELEFRA: (212) 790-9090
TELEFRA: (212) 790-9090
TELEFRA: (212) 790-9090
TELEFRA: (212) 80-864/9741
TELEFRA: (212) 80-864/9741
TELEFRA: (212) 80-864/9741
TELEFRA: (212) 80-864/9741
TELEFRA: (212) 80-864/9741
                          Best Local Similarity 62.3%; Pred. No. 0.00038;
Matches 81; Conservative 0; Mismatches 49;
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1 Similarity 62.3%;
81; Conservative
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345..1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-261-578-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 81
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US-08-261-578-1
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COUNTRY:
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NAME/KEY: In claim 1(vi) starting at triplet in position 201-203
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet in position 201-203
NAME/KEY: and ending at the triplet in position 201-203
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NAME/KEY: and ending at the triplet in position 201-203
NAME/KEY: and ending at the triplet 3018-3020
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NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3020
NAME/KEY: and ending at the triplet 3018-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.6%; Score 50.8; DB 2; Length 3829; 74.4%; Pred. No. 0.00083; tive 0; Mismatches 22; Indels 0
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Patent No. 6160106
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins
FILLE REFERENCE: sequencelist
CURRENT PAPLICATION NUMBER: US/08/810,712G
CURRENT FILING DATE: 1997-03-03
EARLIER APPLICATION NUMBER: PCT/US94/11598
EARLIER PILING DATE: 1994-10-12
NUMBER OF EQ. ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 0.00083;
0; Mismatches 22
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US-08-998-416-595/c
; Sequence 595, Application US/08998416
; Patent No. 6239264.
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APPLICANT: Philippsen, Peter
APPLICANT: Pollmann, Rainer
APPLICANT: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.6%;
Best Local Similarity 74.4%;
Matches 64; Conservative (
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Matches 64; Conservative
not applicable
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; LOCATION: (201)..(3020)
US-08-810-712-6
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3829
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UNITS:
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1254 acacagecegtgeaaegtattttatacaatgetetgaaaateatagteteaatetagaea 1313
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APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.8; DB 4; Length 6
Pred. No. 0.00063;
0; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION: A15

PRIOR APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Medgs, J. Timothy

REGISTRATION NUMBER: PF/5-30306/A/CGC1976

TELEPHONE: 919-541-8587

INFORMATION FOR SEQ ID NO: 595:

SEQUENCE CHARACTERISTICS:

LENGTH: 658 base pairs

TYPE: NUCLEIC acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08342411A; Patent No. 5639616; GENERL INFORMATION:
APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORIGINAL SOURCE:
; ORGANISM: PAG1408RP
US-08-998-416-595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-08-342-411A-1
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Query Match 3.34
Best Local Similarity 74.74
Matches 59; Conservative
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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US-09-248-335-25
; Sequence 25, Application US/09248335
; Sequence 25, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: MCGONIGLE, BRIAN
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT PILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924 759
EARLIER APPLICATION NUMBER: 1997-September-05
NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 25
; LENGTH: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: AROld, White & Durkee
STREET: P.O. BOX 4433
CITY: Houston
STATE: TX
COUNTRY: USA
2TP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER READABLE FORM:
REDIUM TYPE: IBM PC COMPUTER: 1BM PC COMPUTER: 33,928
REPERENCE/DOCKET NUMBER: 33,928
RECEIGNATION NUMBER: 33,928
RECEIGNATION NUMBER: 33,928
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RECEIGNATION 
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Pred. No. 0.0025;
0; Mismatches 3
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Best Local Similarity 68.4%;
Matches 67; Conservative C
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STRANDEDNESS: single
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CRGANISM: maize
US-09-248-335-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
COCATION:
US-08-342-411A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        792 ccatatgtgcaggaggtcatttcaagttgtcgtgagaggaaacggcttccgacatgccc 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            852 gcaacgtggacagggtectctgcagcttcaagatcaatgactcggtcacactcaatgaga 911
                                                                                      1336 attomaatoccagtgtotaacattcaataaatagotatatgaaatcaamaaaaaaaaa 1395
                                                                                                           cch 3.3%; Score 47; DB 1; Length 7218; al Similarity 6.7%; Pred. No. 0.012; 26; Conservative 199; Mismatches 164; Indels
Length 1279;
Score 47; DB 3; Length 127
Pred. No. 0.0049;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: BCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Folley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                        1396 aaaaaaaaaaaaaaaaaa 1414
                                                                                                                                                                                                                  TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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us-09-970-076-1.rni

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Gaps

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Score 46.8; DB 1; Length 1364; Pred. No. 0.0057; 0; Mismatches 22; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,493
FILING DATE: 25-MAR-1996
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
0.0057;
22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                      1328 AAAAAAAAAAAAAAAAAAAAA 1349
                                                                                                                                                                                                                          1393 aaaaaaaaaaaaaaaaaaaaa 1414
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08621493
Patent No. 5723127
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REGISTRATION NUMBER: 31,215
REFERENCE/FOCKET UNBER: WST
TELECOMMUNICATION:
TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
                                                         60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19477
COMPUTER READABLE FORM:
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101..859
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Best Local Similarity
Matches 60; Conserve
     Query Match
Best Local Similarity
Matches 60; Conserv
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; LOCATION:
US-08-621-493-3
                                                                                                                                                                                                                                                                                                                                                                                       US-08-621-493-3
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           972 gcatgaaagctgcactccaggtcagcatgaacgatggcctctcttttatctccagttctg 1031
                                                                                                                                                                                                                                                                                                             1032 tcatcatcaccaccacacactgttctgacggttccatcctggccatcgccctgctgatcc 1091
                                                                                                                                                                                                                                                                                                                                                                                                                       tgttcctgctcctagccctggctctcctcggtggttctggcccctctgctgcactgtga 1151
                                                                                      912 agccettttetgtggaagacaettatttactgtgtccagcgcctatcttaaaagaagttg 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Methods for Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREE: Howson and Howson STREE: Howson and Howson STREET: Spring House Corporate Center, PO Box 457 CITY: Spring House STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 3, Application US/08265087; Patent No. 5571515; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: SCOTE, Phillip APPLICANT: Trinchieri, Giorgio TITLE OF INVENTION: Compositions and Method TITLE OF INVENTION: IL-12 as an Adjuvant NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1371 YYYYYYYYYYYYYYYYYYYYYYYYYYY 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1152 ttatcaaggaggtccctccacccctgcc 1180
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E:
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECHONE: 215-540-9206
TELECHONE: 215-540-9206
TELETHONE: 215-540-9206
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 424
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US-08-265-087-3
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US-08-265-087-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                           TITLE OF INVENTION: Compositions and Methods for Use of
                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWSON and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.3%; Score 46.8; DB 4; Length 1 Best Local Similarity 73.2%; Pred. No. 0.0057; Matches 60; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
FLING DATE: 01. Mar-1999
CLASSIFICATION: <university Company Compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: CURLOWN
FILING DATE: CURROWN
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: 08 08/229,282
FILING DATE: 18-APR-1994
ATORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEPHONE: 215-540-9218
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   IL-12 as an Adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 101..859
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/965,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-1994
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GENERAL INFORMATION:
APPLICANT:
                                                     APPLICANT: Scott, Phillip
Trinchieri, Giorgio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1393 aaaaaaaaaaaaaaaaaaaa 1414
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
tent No. 6168923
GENERAL INFORMATION:
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PCT-US94-12883-3
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      Patent
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Pred. No. 0.0057;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,493
FILING DATE: 25-MAR-1996
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-UN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 31,215
RELEPHONE: 215-540-9206
TELEFAX: 215-540-9206
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-260-173-3
; Sequence 3, Application US/09260173
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                                                     1328 AAAAAAAAAAAAAAAAAAAA 1349
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US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
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ilarity 73.2%;
Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
101..859
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MOLECULE TYPE:
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COCATION:
US-08-965-688-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CONA to mRNA
DESCRIPTION: Tobacco CCaMK cDNA and deduced amino-acid
DESCRIPTION: sequence
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bachettira W. Poovalah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: protein-coding sequence (not including
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Klarquist Sparkman Campbell Leigh
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/323,449
FILING DATE: OCTODER 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: DOW, Alan. E. RGGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-4500
TELECOMMUNICATION INFORMATION:
TELEPRONE: (503) 226-7391
TELEPRONE: (503) 226-7391
TELEPRONE: (503) 226-7391
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 DASS PAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOUTHWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
                                                                                                                                       United States of America
                                                                                                                                                                                                                                                         US-08-655-352-10
; Sequence 10, Application US/08655352
Patent No. 6077991
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
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CORRESPONDENCE ADDRESS:
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; LOCATION:
US-08-655-352-10
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** APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.

** TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION

** OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53

** NUMBER OF SEQUENCES: 58

** CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Score 46.8; DB 5; Length 1: Best Local Similarity 67.3%; Pred. No. 0.0065; Matches 66; Conservative 0; Mismatches 32; Indels
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Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/12883 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHELL
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFRAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                    FILING DATE: CONCULTENTLY HEREWITH CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,003
FILING DATE: 10-NOV-1993
CLASSIFICATION:
                                       E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/171,623
FILING DATE: 22-MAR-1988
                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: DNA (genomic) PCT-US94-12883-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 57.57
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                               Houston
                                                                                                      Texas
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                                         ADDRESSEE:
                                                                                                                      COUNTRY:
                                                          STREET:
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                                                                                                 STATE:
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Search completed: August 9, 2002, 00:23:01 Job time: 7954 sec

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9, 2002, 10:47:01; Search time 31.3 Seconds (without alignments) 697.694 Million cell updates/sec
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DIA1_MOUSE	ZAP3_MOUSE	WAIP_HUMAN	ITAD_HUMAN	APG_BRANA	TEGU_HSVEB	PRP2_MOUSE	EXTN_MAIZE	APG_ARATH	MK07_HUMAN	VP40_HSV11	FYB_MOUSE
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160.5	160.5	159.5	159.5	158.5	158.5	158	157.5	157.5	157.5	157	157
_	22	96	37	38	39	6	4.7	12	43	44	13

ALIGNMENTS

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-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; seem to be produced by alternative splicing.
-!- TISSUE SPECIFICITY: Highly expressed in tumor endothelial cells but not in normal endothelial cells.
-!- DOMAIN: Binding to PA seems to be effected through the VWA domain.
-!- SIMILARITY: BELONGS TO THE ATR FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM 3).

Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; "Identification of the cellular receptor for anthrax toxin."; Nature 414:225-229(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 184-564 FROM N.A. (ISOFORM 1), AND SEQUENCE FROM N.A.
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Vogelstein E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cellular role is not yet known.
-!- SUBUNIT: Binds to the protective antigen (PA) of Bacillus
                                                             ATR HUMAN STANDARD; PRT; 564 AA. 09H6X2; Q9H6X2; Q9NVP3; 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last sequence update) Antrax toxin receptor precursor (Tumor endothelial marker 8). ATR OR TEM8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20407466; PubMed-10947988;
St Croix B., Rago C., Velculescu V., Traverso G.,
Montgomery E., Lal A., Riggins G.J., Lengauer C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genes expressed in human tumor endothelium."; science 289:1197-1202(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2). PubMed=11700562;
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ATR_HUMAN
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(see http://www.isb-sib.ch/announce/
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MISSING (IN ISOFORM 2).
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WVSSTSGFKEGNSHPCLPARPHT (IN ISOFORM 3).
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                                                                                                                               Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing. SIGNAL 1 32 POTENTIAL
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EXTRACELLULAR (POTENTIAL).
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Best Local Similarity 100.0%; Pred. No. 1.6e-176;
Matches 564; Conservative 0; Mismatches 0;
               modified and this statement is not removed.
                         entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      N-LINKED (
EDDD -> NK
                                                                                                                                                                                                                                                                                                                               ISOFORM 4)
                                                                                                                                                                                  POTENTIAL.
                                                     EMBL; AF279145; AAK52094.1; -.
EMBL; AK025429; BAB15128.1; ALT_INIT.
EMBL; AK001463; BAA91707.1; ALT_FRAME.
EMBL; BC012074; AAH12074.1; -.
                                                                                                                                                                                                                                                                                                                                                  62789 MW;
                                                                                                          Interpro: IPR002035; vWFA.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                   564 AA;
                                                                                                                                                              33
322
343
3443
3443
3460
506
1166
1184
262
262
262
268
                                                                                                    606410;
                                                                                                                                                                        DOMAIN
TRANSMEM
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CARBOHYD
                                                                                                                                                                                                                                                                   VARSPLIC
VARSPLIC
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                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                   01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Antrax toxin receptor precursor (Tumor endothelial marker 8).
ATR OR TEM8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE ATR FAMILY. SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                             562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 88-562 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF378762; AAL11999.1; -.
EMBL; AK013005; BAB28591.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-21085660; PubMed=11217851;
564
                                 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer Res. 61:6649-6655(2001).
                 541 PPPPQAPPPNRAPPPSRPPRPSV
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By similarity
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                   ATR_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                             SEQUENCE FROM N.A.

MEDLINE-21539596; PubMed=11683410;

MEDLINE-21539596; PubMed=11683410;

MEDLINE-21539596; PubMed=11683410;

MEDLINE-21539596; PubMed=11683410;

MAXWell S.A., Davis G.E.;

"Differential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.";

J. Cell Sci. 114:2755-2773(2001).

SUBUNIT: Seems to bind to collagen type IV and laminin.

SUBCELLULAR LOCATION: Type I membrane protein (Probable).

SIMILARITY: BELONGS TO THE ATR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYFVEOLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPILLARY MORPHOGENESIS PROTEIN-2 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.0%; Score 1060; DB 1; Length 386; 45.3%; Pred. No. 1.5e-57; ive 58; Mismatches 84; Indels 12:
                                        Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P
0F9B2D6688EAB17A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
01-MAR-2002 (Rel. 41, Last annotation update)
Capillary morphogenesis protein-2 precursor (CMG-2).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                      EMBL; AY040326; AAK77222.1; -. PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.0 Best Local Similarity 45.3 Matches 219; Conservative
                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
211
386 AA;
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216
237
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TRANSMEM
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GRCINFTRVKNSQPAKYPLNNTYHPSSPPAAPIYTPPPPAAP
                                                                                                                                                                                                                                HCPPPAPSAPTPPIPSPPSTLPPPPQAPPPNRAPPPSRPPP
RPSV -> REGWRLTICLGSKHVHPGRHDKGPETPLLKQA
WMFSSFLERAFO (IN ISOFORM 2).
6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPSAPTPPIPSIPSTLPPPPOAPP 548
                                                                                                                                                                                                                                                                                                                                                                                                                                        LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                               LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ 68
                                           Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEESEEDDD
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                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                         (POTENTIAL)
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                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
WPA.
WPA.
POP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
N-LINKED (GLCNAC...) (POTENTIN'-LINKED (GLCNAC...) (POTENTIN'-LINKED (GLCNAC...) (POTENTIN'-LINKED (GLCNAC...) (POTENTIN'-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                     Length 562;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                     ANTRAX TOXIN RECEPTOR
                                                                                                                                                                                                                                                                                                                     Score 2901; DB 1;
Pred. No. 5.4e-169;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                            62308 MW;
                                                                                                                                                                                                                                                                                                                     95.9%;
MGI:1919432; Atr.
rPro; IPR002035; vWFA.
                         VWFA; 1
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                     562
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164
1182
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                                                                                                                                                                                                                                                                            562 AA;
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 538; Conserv
                           PS50234;
                                                                     31
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182
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P58335;
                                          Receptor; SIGNAL
                                                                                 DOMAIN
TRANSMEM
DOMAIN
DOMAIN
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CARBOHYD
                                                                                                                                                                                                    CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                            SEQUENCE
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                            PROSITE;
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DOMAIN
                                                                       CHAIN
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NONTRIPLE-HELLCAL SEQUENCES.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE
                                                                                                                                                                                                                                                                                                                                                 Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H., Nishida Y., Obara M., Kimata K.; The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III molfis, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95370352:

Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;

Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;

"Large and small splice variants of colladen XII: differential
expression and ligand binding";

expression and ligand binding";

-i- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
-i- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINTNG FIBRILS, THE COLL DOMAIN GOULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBRILS, AND THE COLL DAMAINS MAY BE
LOCALIZED IN THE PERFIFIBILLAR MATRIX.

-i- SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF
                                                                                                                                                                                                                                                      Eukaryofa; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                              423 QEYEFPEPRNLINNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVMRPQ 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-1283 FROM N.A. (SHORT FORM), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.; "Type XII collagen. A large multidomain molecule with partial homology to type IX collagen."; J. Biol. Chem. 264:19772-19778(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon M.K., Gerecke D.R., Olsen B.R.; "Type XII collagen: distinct extracellular matrix component discovered by cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The two splice variants of collagen XII share a common Blochim. Blophys. Acta 1171:97-98(1992).
                                                                                                                                                             CAIC_CHICK STANDARD; PRT; 3124 AA. P13944; Q04509; 01-JAN-1990 (Rel. 13, Created) 01-NOV-1997 (Rel. 15, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) collagen alpha 1(XII) chain precursor (Fibrochimerin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
                                                                                                                                                          PRT; 3124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2960-3076 FROM N.A. MEDLINE=87317590; PubMed=3476925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93042014; PubMed=1420368; Trueb J., Trueb B.;
                                                                                                                                                                                                                                                                                                                                      STRAIN-WHITE LEGHORN;
MEDLINE-92011862; PubMed=1918137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90062079; PubMed=2584192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell Biol. 115:209-221(1991).
                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
                                               318 ETEEPIRP
                                                                                               370 EGD 372
                                                                       475 PGD 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2846-2873
                                                                                                                                                  CA1C_CHICK
                                                                                                                                     RESULT
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                                                                                                                                                                                   1- TISSUES SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS,
11GAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE
11GAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE
11SSUES CONTAINING TYPE I COLLAGEN.
11SSUES CONTAINING TYPE I COLLAGEN.
12SUES CONTAINING TYPE I COLLAGEN.
14ELICAL DOMAINS (COLL AND COL2) AND THREE NONTRIPLE-HELICAL
15CAL NOL1, NC2, AND NC3).
15CAL PUM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
15CAL END.
15CAL END.
15CAL END.
15CAL ENDOMAINS AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
15CAL END.
15CAL THE TRIPLE-HELICAL TAIL IS SOME OR ALL OF THE CHAINS.
15CAL END.
15CAL END.
15CAL END.
15CAL ENDOMAINS TO THE FIRELY.
15CAL ELEGANG TO THE FIRELY.
15CAL ENDOMAINS AT WEAD DOMAINS.
15CAL ENDOMAINS AT WHEAD DOMAINS.
15CAL ENDOMAINS AT WHEAD DOMAINS.
15CAL ENDAMENTY: CONTAINS A FIBRONECTIN TYPE III-LIKE DOMAINS.
15CAL ENDAMENTY: CONTAINS A FIBRONECTIN TYPE III-LIKE DOMAINS.
FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      natrix; Connective tissue; Repeat; Hydroxylation; Collagen; Signal; Glycoprotein; Alternative splicing. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLAGEN ALPHA 1(XII) CHAIN
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FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 7
FIBRONECTIN TYPE-III 7
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FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
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EMBL; X61024; CAA43358 1; --
EMBL; M17375; AAA48518 1; --
EMBL; M7375; AAA48518 1; --
EMBL; X67327; CAA47744.1; --
FIR, A28037; A28037.
Interpro; IPR000086; FNIII_repeat.
Interpro; IPR001096; FNIII_repeat.
Interpro; IPR001036; FNIII_repeat.
Interpro; IPR001036; VMFA.
Ffam; PF001391; Collagen; 4.
Ffam; PF001391; Collagen; 4.
Ffam; PF00092; VWF.
Ffam; PF00092; VWF.
FRINTS; EM0014; FNIYPEIII.
PRINTS; EM0014; FNIYPEIII.
PRINTS; SM00164; FNIYPEIII.
PRINTS; SM00164; FNIYPEIII.
PROSITE; PS50234; VWFA.94.
PROSITE; PS50234; VWF
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2643 EVKKIFYGSFHKVHIVVTSSNVKIYIDCSEILEKPIKEAGNITTDGYEILGKLLKGDRRS 2702
                                                                                                                                                                                                                                           2821 PGLPGRSGTPGLPGPPGPPGERGFTGKDGPTGPRGPPGPAGAPGVPGVAGPSGKPGK 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPPSA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELTI H., Mengele R., Wenzi S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of
the cellular compartment.";
J. Cell Biol. 109:3493-3501(198).
-:- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS TH
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (23 STRUCTURE). THE
COVALENT CROSS-LIRKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
-!- FTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
HYDROXYPROLINE RESIDUES.
                                                                                                                                                            2761 GPGAKGPRGERGLTGSSGPPGPRGETGPPGPQGPPGPQGPNGLQIPGEPGRQGMKGDAGQ
                                                                             2703 ATLEIONFDIVCSPVWTSRDRCCDLPSMRDE--AKCPALPNACTCTQDSVGPPGPPGPPG
                                                                                                                      501 -----YHTSSPPPAPIYTPPPAPHCPPPP------YHTSSPPPAPHCPPPP
                                                                                                                                                                                                     526 PSAP----TPPIPSPPSTLPPP-----PPSRPPPR
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14.2%; Pred. No. 3.2e-05;
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                                         469 SVMRPQPGD-----TGRCINFTRVKNNQPAKYP-LNNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AVG-1991 (Rel. 19, Created)
01-AVG-1991 (Rel. 19, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 PTPPIPSPPSTLPPPPQAPPNRAPPPSRPPPRPS 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-F. NAGARIENSIS / HK10;
MEDLINE-90094551; Pubmed-2689458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Sulfation; Hydroxylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Volvocaceae; Volvox.
NCBI_TaxID=3067;
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Best Local Similarity
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P21997;
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SEQUENCE
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SSGP_VOLCA
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                                                                                                                                                                                           WITH 2 THELLICAL REGION (COLI)
WITH 2 THELLICAL REGION (NCI).

ASP/GLURCH (ACIDIC).

ARG/LYS-RICH (BASIC).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

MISSING (IN SHORT ISOFORM).

T -> S (IN REF. 4).

P -> F (IN REF. 2).

L -> F (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :602 QITDRDYKPQVGV------VLDPGSKVLSFFNKDIRGEVQTVTFD----ND
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                                                                                                                      TRIPLE-HELICAL REGION (COL2) WITH 1 IMPERFECTION.
                                                                                                                                                            NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
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094285AFE7F346CF CRC64;
                                                            FIBRONECTIN TYPE-III 18.
  FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 17.
                                                                                                 NONHELICAL REGION (NC3)
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2901
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Hydroxylation.
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Q05859;
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01-JUN-1994
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                                                                                                                                                                                                                           Query Match
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FM14_MOUSE
                                                                                                                                                                                                                                                                                                                                                                      469
                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                              임
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                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a proline-rich 33-kDa protein.";
c. Natl. Acad. Sci. U.S.A. 82:4399-4403(1985).
FUNCTION: STRUCTURAL COMPONENT IN PRIMARY CELL WALL.
SUBCELLULAR LOCATION: EXTRACALLULAR MATAIX.
PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE
SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                             502 HTSSPPPAPIYTPPPPAPHCPPPPPSAPTPPIPSPPSTLPPPPQAPPPNRAPPPSRPPPR 561
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90147742; pubmed=2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Bakalara in 'Northebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Biochem. Biophys. Res. Commun. 166:66-73(1990).
PIR: A34043; A34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carrot extensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daucus carota (Carrot).
Enkaryota Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                      Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECTENCE FROM N.A. Chen J., Varner J.E.;
Chen J., Varner J.E.;
"An extracellular matrix protein in plants: characterization of genomic clone for carrot extensin.";
EMBO J. 4:2145-2151(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                         H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen J., Varner J.E.;
"Isolation and characterization of cDNA clones for and a proline-rich 33-kha mrotoir."
                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                    6.5%; Score 197.5; DB 1
58.3%; Pred. No. 9.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 29, Last annotation update)
                                                                                        P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1995 (Rel. 32, Last annotation update)
                                                                                                                                    Hypothetical proline-rich protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AA
     273 POPPSPRAPPSPS 307
                                                                             141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                               POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                             PRT;
                                                                                                                                                                                                                                                                                                       Hypothetical protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                58
116
                                                                                                                                                                                                                                                                                                                                                        141
                                                                                                                                                                                                                                                                                                                                                                     141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extensin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 35; Conserv
                                                                                                                                                  Owenia fusiformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4039;
                                                                                                                                                                                      NCBI_TaxID=6347;
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01-JAN-1988 (
01-JUN-1994 (
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                                                                                 PRO_OWEFU
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NON_TER
SEQUENCE
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A variant limb deformity transcript expressed in the embryonic mouse
limb defines a novel formin.";
Genes Dev. 6:29-37(1992).
- FUNCTION: IS IMPORTANT IN THE MORPHOGENESIS OF LIMB AND MAY HAVE A
- FUNCTION: IS IMPORTANT IN THE MORPHOGENESIS OF LIMB AND MAY HAVE A
- FUNCTION IN DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING
FUNCTION IN DIFFERENTIATED STAFES.
- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; IA (AC Q05860), IB (AC
- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; IA (AC Q05860), IB (AC
- MANNO DIFFERENT TISSUES AND DIFFERENT SESSUE
- TISSUE SPECIFICITY: IT IS FOUND THROUGHOUT THE EMBRYO BUT
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DEVELOPMENTAL STAGE: THIS IS THE ISOFORM FOUND IN THE APICAL
ECTODERMAL RIDGE AND THE MESENCHYMAL COMPARTMENT OF THE DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 KEVPPP---PAEESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409 KLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPP-- 526
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 -KYKYKSPPPPPPVYKYKSPPP------PTPVYKYKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%; Score 191.5; DB 1; Length 306;
26.1%; Pred. No. 5.3e-05;
Live 18; Mismatches 56; Indels 93;
                                                                                                                                                                                                                                                                EMBL; X02873; CAA26632.1; -.
EMBL; M1221; AAA33137.1; -.
PIR; A24354; A24354.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 ---SAPTPPIPSPPSTLPPPP----QAPPPNRAPPP---SRPPPR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 YKYKSPPPPMHSPP---PPTPVKYKSPPPPMHSPPPVYSPPPPK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTENSIN.
AEC944007F0938DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 КЅРРРКНЅРАРЕННҮКҮКЅРРРРКНГРАРЕННУ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Formin 1 isoform IV (Limb deformity protein).
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MEDLINE=92112033; PubMed=1339380;
                                                                                                                                                                                                                                                                                                                                                                                                                                          32
306 EX
34225 MW;
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(Rel. 29, Last sequered) (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 26.19
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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DOMAIN
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    RANGE STATE 
                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 WGEKGSTEEGAKLEKA-KNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 LWVLLRKGYDRVSVMRPQPGDTGR------CINFTRV---KNNQPAKYPLNNAYH 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Gaps
                  -i- PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.
-i- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-i- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-i- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 188.5; DB 1; Length 1206; Pred. No. 0.0004; 39; Mismatches 76; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Developmental protein; Alternative splicing; Phosphorylation; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4DFB38CB52BD8EE7 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Formin 1 isoforms I/II/III (Limb deformity protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIPSPPSTLPPPPQAPPP-----NRAPPPSRPPRP 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FH1 (PRO-RICH).
FH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                 EMBL; X62379; CAA44244.1; -.
PIR; S24407; S24407.
MGD; MGI:101815; Fm..
InterPro; IPR003104; FH2.
InterPro; IPR001265; Formin.
Pfam; PF02181; FH2; 1.
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1043 111
635 63
751 75
1206 AA;
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Best Local Similarity
Matches 69; Conserv
LIMB BUD
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Q05860;
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SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).

CC - FUNCTION: IS IMPORTANT FOR THE MORPHOGENESIS OF LIMB AND KIDNEY
AND MAY HAVE A FUNCTION IN DIFFERENTIATED CELLS OR MAY BE
INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.

CC -- SUBCELLIGHAR LOCATION: Nuclear.

CC -- SUBCELLIGHAR LOCATION: Nuclear.

II, III AND IV (AC 005899); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -- SIMILARITY SPLICING IS SEEN AMONG DIFFERENT TISSUES AND
DIFFERENT SIZE TRANSCRIPES EXIST MITHIN ANY ONE TISSUE AND
DIFFERENT SIZE TRANSCRIPES EXIST MITHIN ANY ONE TISSUES

C -- TISSUE SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY, TESTIS,
LIMB, OVARY, BRAIN, SMALL INTESTINE, SALIVARY GLAND AND HARDERIAN

C -- DEVELOPMENTAL STAGE: IN THE DEVELLOPING LIMB BUD, THE PROTEIN

C -- DEVELOPMENTAL STAGE: IN THE DEVELLOPING LIMB BUD, THE MESENCHYMAL

C COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR REGION. DURING
KIDNEY MORPHOGENESIS, EXPRESSION IS INITIALLY RESTRICTED TO
THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS.

C -- SIMILARITY: CONTAINS I FORMIN HOMOLOGY PAMILY. CAPPUCCINO
SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO
SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION.
MEDLINE=93296176; PubMed=8516300;
Vogt T.F., Jackson-Grusby L., Rush J., Leder P.;
"Formins: phosphoprotein isoforms encoded by the mouse limb deformity
                                                                                      Woychik R.P., Maas R.L., Zeller R., Vogt T.F., Leder P.; "'Pormins: proteins deduced from the alternative transcripts of the limb deformity gene"; Ilimb deformity gene"; Nature 346:850-853(1990).
                                                                                                                                                                                                                                             ÀLTERNATIVE SPLICING.
MEDILINE-97224459; PubMed-9119367;
WANG C.C., Chan D.C., Leder P.;
"The mouse formin (Fmn) gene: genomic structure, novel exons, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METR. S11515; S11515.
METR. S11515; S11515.
METR. S1101815; Fmn.
InterPro: IPR003104; FH2.
Pfam: PF02181; FH2: 1.
PRINTS; PR00828; FORMIN.
SNART: SN00498; FF12: 1.
Nuclear protein; Developmental protein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL).
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SEQUENCE FROM N.A.
TISSUE=Kidney, and Testis;
MEDLINE-90363291; Pubmed-2392150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X53599; CAA37668.1; -.
                                                                                                                                                                                                                                                                                                                                                                       genetic mapping.";
Genomics 39:303-311(1997).
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send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Biochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL PRELIMINARY SEQUENCE FROM N.A.

AGAIT W.S., Apt K.E.;

"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins.";

Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).

-:- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                    TSS------CP--PPPAPIYTPPPPAPH-------CP--PPPPSAPTP 531
                                                                                                                                                                                                                                                                                                                                                    398 WGEKGSTEEGAKLEKA-KNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDA 456
                                                                                                                                                                                                                                                                                                       ----KKKWPTVDASYYGGRGVGGIKRMEVR 397
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                       LWVLLRKGYDRVSVMRPQPGDTGR------CINFTRV---KNNQPAKYPLNNAYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPI_CHLRE STANDARD; PRT; 555 AA.
Q9FPQ6; Q03927;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                               97;
                                                                                                                                                                                                                                              DB 1; Length 1468;
                                                                                                                                                 Indels
                        MISSING (IN ISOFORM IB).
MASSING (IN ISOFORM II).
IA -> SV (IN ISOFORM III).
MISSING (IN ISOFORM III).
MRISSING (IN ISOFORM III).
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PubMed=11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                           532 PIPSPPSTLPPPPQAPPP-----NRAPPPSRPPRP 562
                                                                                                                                                                                                                                                                                                                                                                                                            920 PIPVPSDGPPPPPPPPPPNVLALPNSGGPPPPPPPP 960
                                                                                                             -!- SUBUNIT: Associates with GP2 and GP3.
                                                                                                                                                                             PPPPAEESEEEDDDGLP------
              977 981 E
1252 1287 N
625 722 N
626 627
628 1468 A3; 163809 M
                                                                                                                                                   Conservative
                                                                                                                                    Local Similarity
nes 69; Conserv
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                                 VARSPLIC
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Matches
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last paramotation update)
Wiskott-Aldrich syndrome protein family member 2 (WASP-family protein member 2) (Verprolin homology domain-containing protein 2).
WASF2 ON WAVEZ OR SCAR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                    VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
N-LINED (GLCNAC. . .) (POTENTIAL).
W-LINED (GLCNAC. . .) (POTENTIAL).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=T-cell lymphoma; MEDLINE=99310608; PubMed=10381382; Suetsugu S., Miki H., Takenawa T., Identification of two human WAVE/SCAR homologues as regulatory molecules which associate with the Arp2/3 (Piochem. Blophys. Res. Commun. 260:296-302(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 187.5; DB 1;
Pred. No. 0.00019;
4; Mismatches 19;
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                              EMBL; M58496; AAA69706.1; ALT_SEQ
GlycoSuiteDB; Q9FPQ6;
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                                                                                                                                                                                                                                                      Signal.
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EMBL; AF309494; AAG45420.1;
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SIGNAL 1 29
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555 AA;
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S -> P (IN REF. 1).

S -> P (IN REF. 1).

R -> G (IN REF. 1).

P -> PP (IN REF. 1).

P -> PP (IN REF. 1).

I -> V (IN REF. 1).

I -> V (IN REF. 1).

C -> R (IN REF. 1).

C -> R (IN REF. 1).

C -> R (IN REF. 1).

M -> R (IN REF. 1).

M -> R (IN REF. 1).

M -> R (IN REF. 1).

M -> R (IN REF. 1).

M -> R (IN REF. 1).

M -> D (IN REF. 1).

SF313599FDF63A6B CRC64;
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T -> K (IN REF. 1).
K -> E (IN REF. 1).
R -> K (IN REF. 1).
I -> M (IN REF. 1).
F -> TS (IN REF. 1).
S -> P (IN REF. 1).
S -> GP (IN REF. 1).
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                                                                                                          InterPro; IPR003124; WH2.
                                                                                                                    Pfam; PF02205; WH2; 1.
SMART; SM00246; WH2; 1.
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497
497 AA;
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93
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DOMAIN 20
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                                                                                                                                             356 PPPAEESEEEDDDGLPKKKWPTVDASYY-----GGRGVGGIKRMEVRWGEKGSTE 405
                                                                                                                           406 EG-----AKLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWV 459
                                                                                                                                                                                                          502 HTSSPPPA-PIYTP-----PPPAPHCP---------PPPSAPT- 530
                                                                                           130 PPPLNNLTPYRDDGTEALKFYT-DPSYFFDLWKKKMLQDTRDIMKEKRKH-RKEKKDNPN 187
                                    Gaps
                                                                                                                                                                                       LLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPA-----KYPLNN------AY
                                92;
6.2%; Score 187; DB 1; Length 497; 26.5%; Pred. No. 0.00018; ive 27; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                               -----PPIPSPPS----TLPPPPQAPPNRAPPPSRPPP 560
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                 Best Local Similarity
Matches 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Extracellular matrix.
PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 KNNQPAKYPLNNAYHTSSPPPAPIYTPPPPA------------PHCPPP 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 PEPRNLINNMARRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTRV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                  sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                          Extensin precursor (Cell wall hydroxyproline-rich glycoprotein). HRGPNT3.
                                                                                                                                                                            6.1%; Score 185.5; DB 1; Length 620;
29.7%; Pred. No. 0.00028;
ive 10; Mismatches 34; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTAINS THE SER-PRO(4) REPEATS.

3 X APPROXIMATE TANDEM REPEATS.
641DD2278AB28524 CRC64;
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Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
Hydroxylation.
                                                 Last sequence update)
Last annotation update)
          620 AA.
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                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seq
16-ocr-2001 (Rel. 40, Last ann
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148
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229
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205
620 AA;
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Matches 52; Conserv
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         EXTN_TOBAC
P13983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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EXTN_TOBAC
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Kwan S.P., Hagemann T.L., Radike B.E., Blaese R.M., Rosen F.S.;
Identification of mutations in the Wiskott-Aldrich syndrome gene and
characterization of a polymorphic dinucleotide repeat at DXS6940,
adjacent to the disease gene.";
Proc. Natl. Acad. Sci. U.S.A. 92:4706-4710(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kolluri R., Shehabeldin A., Peacocke M., Lamhonwah A.-M., Teichert-Kuliszewska K., Weissman S.M., Siminovitch K.A.; "Identification of WASP mutations in patients with Wiskott-Aldrich syndrome and isolated thrombocytopenia reveals allelic heterogeneity
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MEDLINE-96133286; PubMed-8528199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hagemann T.L., Kwan S.-P.;
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Derry J.M.J., Ochs H.D., Francke U.;
"Isolation of a novel gene mutated in Wiskott-Aldrich syndrome.";
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derry J.M.J., Kerns J.A., Weinberg K.I., Ochs H.D., Volpini V., Estivill X., Walker A.P., Francke U.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS WAS K-31; M-75; P-82; C-86; H-86; C-97; K-133; E-476
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VARIANTS WAS TRP-43; MET-45; MET-75 AND CYS-86
                                                 P42768; QGUNJ9; CONTROL OF THE CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CO
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Derry J.M.J., Ochs H.D., Francke U.;
Cell 79:923-923(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at the WAS locus.";
Hum. Mol. Genet. 4:1119-1126(1995).
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MEDLINE=99167346; Pubmed=10066431;
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MEDLINE=95273432; PubMed=7753869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 78:635-644(1994)
                                                                                                                                                                                                                                                         Homo sapiens (Human)
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El-Hakeh J., Rosenzweig S., Oleastro M., Danielian S.;
Molina F., Rivas E.M., Zelazko M., Danielian S.;
Molina F., Rivas E.M., Zelazko M., Danielian S.;
novel. mutattons: "18 and the syndrome in Argentina: 17 unique, including nine
novel. mutattons: Possible Regularor Perhyphoryte and Platelet Function.
-: PUNCTION: POSSIBLE REGULATOR PETHWAYS WITH CYPOSKELETAL FUNCTION.
-: FUNCTION: POSSIBLE REGULATOR PATHWAYS WITH CYPOSKELETAL FUNCTION.
-: SUBBUNT: BINDS TO CDG42, RAC, NCK, FYN, SRC KINASE FGR, BTK, ABL,
MIP, AND TO THE P85 SUBBUIT OF PLC-GAMMA.

-: TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE THYMUS. ALSO
FOUND, TO A MUCH LESSER EXTENT, IN THE SPLEEN.
-: DOMAIN: THE WHI (WASP HOMOLOGY 1) DOMAIN MAY BIND A PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITINE-99378988; PubMed-9713366; M. Notarangelo L.D., Giliani S., Facchetti F., Blanzuoli L., Vormi W., Notarangelo L.D., Giliani S., Fiorini M., Fasth A., Stewart D.M., Nelson D.L.; "Defective actin polymerization in EBV-transformed B-cell lines from patients with the Wiskott Aldrich syndrome.";
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MEDLINE=99374925; PubMed=10447259;
Lemahleu V., Gastier J.M., Francke U.;
"Novel mutations in the Wiskott-Aldrich syndrome protein gene and
their effects on transcriptional, translational, and clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [11]
MEDLINE=98350091; PubMed=9683546;
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MacCarthy Morrogh L., Gaspar H.B., Wang Y.-C., Katz F., Thompson I Layton M., Jones A.M., Kinnon C.;
Layton M., Jones A.M., Kinnon C.;
"Absence of expression of the Wiskott-Aldrich syndrome protein in peripheral blood cells of Wiskott-Aldrich syndrome patients.";
clin. Immunol. Immunopathol. 88:22-27(1998).
                                                                                                                                                                                                                                                                                                                          Ariga T., Yamada M., Sakiyama Y.;
"Mutation analysis of five Japanese families with Wiskott-Aldrich syndrome and determination of the family members' carrier status using three different methods.";
MEDLINE=97272113; PubMed-9126958;
Remold-O'Donnell E., Cooley J., Shcherbina A., Hagemann T.L.,
Kwan S.-P., Kenney D.M., Rosen F.S.;
"Variable expression of WASP in B cell lines of Wiskott-Aldrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ή.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98092074; PubMed-9445409; Parolini O., Ressmann G., Haas O.A., Pawlowsky J., (Rnapp W., Holter W.; "X-linked Wiskott-Aldrich syndrome in a girl."; New Engl. J. Med. 338:291-295(1998).
                                                                                                                                                                                                                                                                     VARIANTS WAS LYS-31 AND MET-45.
MEDLINE=97253413; PubMed=9098856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS WAS HIS-52 AND TRP-70.
                                                                                                                                                                    syndrome patients.";
J. Immunol. 158:4021-4025(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Calcium-dependent cell-adhesion protein. Essential for maintenance of normal retinal and cochlear function.
SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).
TISSUE SPECIFICITY: Expressed in brain, lung, kidney, spleen and restis. Found also in the inner and outer synaptic layers, and the nerve fiber layer in adult and fetal retinas. Found in the supporting cells, outer sulcus cells and spiral ganglion of fetal
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Fetal brain;
MEDLINE-21380012; PubMed-11487575;
Alagramam K.N., Yuan H., Kuehn M.H., Murcia C.L., Wayne S.,
Alagramam K.N., Yuan H., Kneus R., Van Laer L., Bernier F.P.,
Srisailpathy C.R.S., Lowry R.B., Knaus R., Van Laer L., Bernier F.P.,
Schwartz S., Lee C., Morton C.C., Mullins R.F., Ramesh A.,
Van Camp G., Hagemen G.S., Woychik R.P., Smith R.J.H.;
"Mutations in the novel protocadherin PCDH15 cause Usher syndrome type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: Defects in PCDH15 are the cause of Usher syndrome type 1F (USH1P). Usher syndrome type 1 is a autosomal recessive disorder characterized by congenital profound sensorineural hearing loss, constant vestibular dysfunction and prepubertal onset of retinitis spignentosa leading to blindness. Usher syndrome is the most common cause of combined deafness and blindness in developed countries. SIMILARITY: CONTAINS I CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11398101;
Ahmed Z.M., Rlazuddin S., Bernstein S.L., Ahmed Z., Khan S.,
Griffith A.J., Morell R.J., Friedman T.B., Rlazuddin S., Wilcox E.R.;
"Mutations of the protocadherin gene PCDH15 cause Usher syndrome type
                  Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                         PCTS_HUMAN STANDARD; PRT; 1955 AA. 0960U1; 0960T8; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Protocadherin 15 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet. 10:1709-1718(2001).
                                                                                                        381 LPPPPPGAGGPPMPPPPPPPPP 405
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Plam; PF00228; Cadherin; 10.
PROSTIE; PS00232; CADHERIN_1; 3
PROSITE; PS50268; CADHERIN_2; 10.
                                                                       -LPPPPQAPPNRAPPSRPPRPS
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MIM; 605514; -.
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PC15_HUMAN
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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/FTId=VAR_008106
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/FTId=VAR_012711
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EMBL; U18935; AAA60381.1; -.
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                                                                                                                                                                            AF115549; AAD26691.1; -. AF196970; AAF06804.1; -.
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Pfam; PF00568; WH1; 1.
Pfam; PF02205; WH2; 1.
SMART; SM00285; PBD; 1.
SMART; SM00461; WH1; 1.
SMART; SM00461; WH1; 1.
RPGSTTE; PS50108; GBD; 1.
RPGPAT; Dissemutation.
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InterPro; IPR000697:
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         Signal; Multigene family; Vision; Deafness; Retinitis pigmentosa;
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(POTENTIAL)
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01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
circumsporozoite procurs (CS).
Plasmodium berghei (strain Anka).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 182; DB 1; Length 1955; 28.9%; Pred. No. 0.0017;
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L -> Q (IN REF. 2).

Q -> R (IN REF. 2).

Q -> R (IN REF. 2).

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CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
CADHERIN 7.
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CADHERIN 10.
CADHERIN 10.
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P23093;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- MISCELLEMENOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-:- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
SUPPLIES FROM N.A. banded=2183186; Subribler A., Sinden R.E.; Lockyer M.J., Davies C.S., Subribler A., Sinden R.E.; Lockyer M.J., Davies C.S., Subribler A., Sinden R.E.; Lockyer M.J., Davies C.S., Subribler A., Subribler Berghei circumsporozoite "Nucleotide sequence of the Plasmodium berghei circumsporozoite protein gene from the Anka clone 2.34L."; Nucleic Acids Res. 18:376-376(1990).

1. FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODMINANT SUBRACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE SUBRACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE PARASITE THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEAT SEQUENTED FOR THE REPEA
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17 X 2 AA REPEATS OF P-Q.
0EC240EE35681AF8 CRC64;
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SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
23
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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Job time: 827 sec
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347 AA;
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August 9, 2002, 10:47:04; Search time 31.3 Seconds (without alignments) 411.936 Million cell updates/sec
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1728
1 MATAERRALGIGFOWLSLAT.....TTHCSLHKIASGPTTAACME 333
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      105224 seqs, 38719550 residues
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Post-processing: Minimum Match 0% '
Maximum Match 100%
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		homo sapien	mus musculu	homo sapien	homo sapien	homo sapien	homo sapien	gallus gall	mus musculu	mus musculu	mus musculu	homo sapien	gallus gall	caenorhabdi	homo sapien	notophthalm	gallus gall	homo sapien	homo sapien	homo sapien	mus musculu	mus musculu	mus musculu	mus musculu	mus musculu	homo sapien	gallus gall	homo sapien	homo sapien	oryctolagus	drosophila	borrelia bu	=	homo sapien
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SUMMARIES	Ţ	ATR_HUMAN	ATR_MOUSE	CMG2_HUMAN	ITAD_HUMAN	ITAM_HUMAN	ITAX_HUMAN	CA1C_CHICK	ITAM_MOUSE	CA1C_MOUSE	CO2_MOUSE	CA1C_HUMAN	CA1E_CHICK	YNX3_CAEEL	CAMA_HUMAN	CA1C_NOTVI	MTN3_CHICK	MTN2_HUMAN	CFAB_HUMAN	CA17_HUMAN	CFAB_MOUSE	CA26_MOUSE	CAMA_MOUSE	MTN4_MOUSE	MTN2_MOUSE	ITAH_HUMAN	CAMA_CHICK	MTN4_HUMAN	MTN3_HUMAN	CA1C_RABIT	ROP_DROME	- 1	TRAP_PLAFA	CA26_HUMAN
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P12111 homo sapien P58079 caulobacter	Q9kOn4 neisseria m Q90615 gallus gall	P15989 gallus gall P38570 homo sapien	060677 mus musculu	09nx02 homo saplen	P18614 rattus norv	043405 homo sapten
CA36_HUMAN HUTI_CAUCR	DNAK_NEIMB ITA1_CHICK	CA36_CHICK	ITAE_MOUSE	NAL2_HUMAN	ITA1_RAT	COCH_HUMAN
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ALIGNMENTS

	ATE_HUMAN ATE_HUMAN STANDARD; PRT; 564 AA.	USHNAX; USHNYS; 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Antrax toxin receptor precursor (Tumor endothelial marker 8).	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		_	RAY Enabled-InfoDeb. Worldge J., Mourez M., Collier R.J., Young J.A.T.; RT Radley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; RT Identification of the cellular receptor for anthrax toxin."; R. Nature 414:225-229(2001).	RP SEQUENCE OF 184-564 FROM N.A. (ISOFORM 1), AND SEQUENCE FROM N.A. (ISOFORM 3).		- w ⊟ v	Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases!- FUNCTION: Cellular role is not yet known!- SUBMIT: Binds to the protective antigen (PA) of Bacillus	-:- SUBCELLULAR LOCATION: Type I membrane protein (Probable):- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; seem	-:- TISSUE SPECIFICITY: Highly expressed in tumor endothelial cells but not in normal endothelial cells:- DOMAIN: Binding to PA seems to De effected through the VWA domain:- SIMILARITY: BELONGS TO THE ATR FAMILY:- SIMILARITY: CONTAINS 1 VWFA DOMAIN.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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coved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                Glycoprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                     WVSSTSGFKEGNSHPCLPARPHT (IN ISOFORM
                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
EDDD -> NKIK (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antrax toxin receptor precursor (Tumor endothelial marker 8). ATR OR TEMM.
                                                                                                                                                                                                                                                                                  Length 564;
                                                                                                                                                   ASP/GLU-RICH (HIGHLY ACIDIC). PRO-RICH.
                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                           B118A00AD5DF2233 CRC64;
                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                     (IN ISOFORM 4)
                                                                                                                                                                                                                              MISSING (IN ISOFORM 3)
                                                                                                              ANTRAX TOXIN RECEPTOR
                                                                                                                                                                                                                                                                                  Query Match 95.4%; Score 1649; DB 1; I Best Local Similarity 100.0%; Pred. No. 2.8e-128; Matches 318; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 AA.
    and this statement is not removed.
           entities requires a license agreement (8 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               ISOFORM 4)
                                                                                                                                 POTENTIAL
                                  EMBL; AF279145; AAK52094.1; -. EMBL; AK025429; BAB15128.1; ALT_INIT. EMBL; AK001463; BAA91707.1; ALT_FRAME. EMBL; E012074; AAH12074.1; -.
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                                                                         InterPro; IPR002035; vWFA.
                                                                                  SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                 Receptor; Transmembrane; SIGNAL 1 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RP SEQUENCE OF 88-562 FROM N.A. (ISOFORM 2).

RX RANIN-C57BL/63; TISSUB=Embryo;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Rondo S., Yammaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yammaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadcta K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadta K., Okazaki Y., Matudo I., Hasido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schimul L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

RA Blake J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazaralli J., Mondberts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Myashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wyashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
GRCINFTRYKNSQPAKYPLNNTYHPSSPPPAPIYTPPPPAP
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                        xinzler K.W., St Croix B.;
rcell surface tumor endothelial markers are conserved in mice
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                                                                                                                                                                                              [1] SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-21443268; PubMed-11559528;
Carson-Walter E.B., Warkins D.N., Nanda A., Vogelstein
Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
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-!- SIMILARITY: BELONGS TO THE ATR FAMILY.
-!- SIMILARITY: CONTAINS 1 WWFA DOMAIN.
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EMBL; AK013005; BAB28591.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Res. 61:6649-6655(2001).
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InterPro; IPR002035; vWFA.
PROSITE; PS50234; VWFA; 1.
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SEQUENCE FROM N.A.
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                                                                                                                                                          ö
HCPPPAPSAPTPPIPSPPSTLPPPPQAPPNRAPPPSRPPP
                    RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA
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basement
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                                                                                                                                                                                                                                                                                                                                                                                                                               189 ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 ARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS 308
                                                                                                                                                                                                                                                                        69 LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                                                        Gaps
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                                                                                                                                                                                             9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-2153956; PubMed-11683410;
A Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.A., Davis G.E.;
Maxwell S.A., Davis G.E.;
T collagen matrices: regulated expression of genes involved in base membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.";
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J. Cell Sci. 114:2755-2773(2001).
J. Cell Sci. 114:2755-2773(
                                                                                                                                                        ;
                                                                                                                    Length 562;
                                        WMFSSFLERAFQ (IN ISOFORM 2).
6AC92049B4B4F7C CRC64;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Capillary morphogenesis protein-2 precursor (CMG-2).
Homo sapiens (Human).
                                                                                                                 Score 1553; DB 1;
Pred. No. 2.2e-120;
5; Mismatches 7;
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                                                        62308 MW;
                                                                                                                 89.9%;
96.1%;
                                                                                                                 Query Match 89.9
Best Local Similarity 96.1
Matches 298; Conservative
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P58335;
                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
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"A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                      63 YYEVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
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MEDLINE=96111956; PubMed=8777714;
Wan der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
Staunton D.E., alnha d beta 2, binds preferentially to IC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                POTENTIAL)
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                         CAPILLARY MORPHOGENESIS PROTEIN-2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                        Length 386;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                             N-LINKED (GLCNAC. ..) (
0F9B2D6688EAB17A CRC64
                                                                                                                                                                                                                                                                                           57;
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                                                                                                                                                                                                                                           : 551.5; DB
No. 4e-38;
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                                                                                                                                                                                                                                                                                           38; Mismatches
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Pred.
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53.8%;
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                                                                                                                                                                                                                                                Query Match 31.9%
Best Local Similarity 53.8%
Matches 114; Conservative
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REPEAT
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     ASSOCIATES WITH BETA-2.

ASSOCIATES WITH BETA-2.

ASSOCIATES WITH BETA-2.

SUBCELULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL

TISSUE SPECIFICITY: EXPRESSED MODERATES AND STRONGLY ON

LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGLY ON

TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN

ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP WACROPHAGES.

DOMAIN: THE INTEGRIN LOMAIN (INSERT) IS A WHFA DOMAIN. INTEGRINS

WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

SIMILARITY: GLONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                                       BORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES FROM THE BLOOD.
                                                                                                                                                                         SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; WRPA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Repeat; Calcium;
as an alternative ligand for vascular cell adhesion molecule (VCAM-1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTEGRIN ALPHA-D.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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FG-GAP 2.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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EMBL, U40274; AAB60634.1; --
EMBL, U40275; AAB60635.1; --
EMBL, U40277; AAB60637.1; --
EMBL, U40279; AAB60638.1; --
EMBL, U40279; AAB60638.1; --
EMBL, U40278; AAB60638.1; --
EMBL, AF187881; AAF62875.1; --
HSSP, P11215; 1A8X.
MIN, 602453; --
InterPro, IPRO00413; Integrin_alpha.
                              J. Exp. Med. 188:2187-2191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR002035; vWFA.
Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00392; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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                                                    INTERACTION WITH VCAM1
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1101
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SIGNAL
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Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
"The human leukocyte adhesion glycoprotein Mac-1 (complement receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1999 (Rel. 11, Created)
01-JUL-1996 (Rel. 34, Last sequence update)
01-OCT-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CE-3 alpha chain) (CDllb) (Leukocyte adhesion receptor MO1)
ITGAM OR CR3A OR CD11B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 FQGPTARQELNTISSAPPQDHVFKV-DNFAALGSIQKQLQEK----1YAVEGTQSRASSS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 ERASEQIYYENRQGYRTA-SVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 LTVVTQLFHHKNGARKSAKKILIVITDGQKYKDPLEYSD-VIPQAEKAGIIRYAIGVGHA 290
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                           POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 L -> V (IN REF. 2).
84 V -> A (IN REF. 2).
126885 MW; F296AlA35455D77D CRC64;
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MEDLINE-93123748; PubMed=8419480;
Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
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MEDLINE-95171458; PubMed=7867070;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
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MEDLINE-92073318; PubMed=1683702;
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MEDLINE-98362595; Pubmed-9687375;
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MEDLINE-88257215; PubMed-2454931;
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DATABAGE: NAME-PROW: NOTE-CD guide CD11b entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J04145;
S52227;
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S52170;
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                                                                                                                                                                          assessment.
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EMBL;
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AAB24821.1;

AAB24821.1;

S52219; S52220;

S52216;

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SEQUENCE FROM N.A.
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 FTFKEFONNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR-----IADS--KDHVFP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 DGEKFGDPLGYEDVIPEADRE---GVIRYVIGVGDAFRSEKSROELNTIASKPPRDHVFQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
11-MAR-2002 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prosite; ps00242; invegrin_Alpha; 1.
PROSITE; Ps50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; 3D-structure; Repeat; Magnesium; Calcium.
Signal; 3D-structure; Repeat; Magnesium; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.4%; Score 145.5; DB 1; Length 1152;
26.2%; Pred. No. 0.00044;
Ive 45; Mismatches 81; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FG-GAP 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
                      EMBL, 552221; AAB24821.1; JOINED. EMBL; 552222; AAB24821.1; JOINED. EMBL; M76724; AAB24821.1; JOINED. EMBL; M76724; AAB58410.1; EMBL; M8477; AAA51960.1; PTR, A31108; RWHUIB. PTR, A3108; A26091; A260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01839; FG-GAP; 5.
Pfam; PF01839; FG-GAP; 5.
Pfam; PF000357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWRADOMAIN.
SNART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1JLM; 11-JAN-97.
Carbbank; CCSD:33581; -.
Carbbank; CCSD:33582; -.
Carbbank; CCSD:33584; -.
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1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 120980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REALINE-87167596; PubMed-3549901;

REDLINE-87167596; Mibbe M., Springer T.A.;

Mibler L.J., Wiebe M., Springer T.A.;

RT mid alpha subunit N-terminal sequences of human Mac-1

RT and pl50,95 leukocyte adhesion proteins.";

LJ. Immunol. 138:2381-2383(1987).

R. J. Immunol. 138:2381-2383(1987).

R. J. Immunol. 138:2381-2383(1987).

RECORNIES THE SEQUENCE G-P-R IN FIBRINGEN. IT MEDIATES CELL-CELL

RECORNIES THE SEQUENCE G-P-R IN PIBRINGEN. IT IS ESPECIALLY

C. INTERACTION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY

MADORYANT IN MONOCYTE ADHESTON AND CHEMOTAXIS.

IMPORTANT IN MONOCYTE ADHESTON AND A BETA SUBUNIT. ALPHA-X

ASSOCIATES WITH BETA-2.

1 SUBUNIT: REPERSORIES TO I membrane protein.

1 SESUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=88166645; PubMed=3327687; COTDI N.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; COTDI A.L., Milling and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                             Corbi A.L., Garcia-Aguilar J., Springer T.A.; "Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
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InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
Pfam: PF01839; FG-GAP: 5.
Pfam: PF00357; integrin_A; 1.
Pfam; PF00092; vWa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  p150,95 molecule.";
J. Biol. Chem. 265:2782-2788(1990)
                                                                                                                                                                                                                                                                                           MEDLINE=90153906; PubMed=2303426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P11215; 1A8X.
CarbBank; CCSD:33581; -.
CarbBank; CCSD:33582; -.
CarbBank; CCSD:33584; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 NPLSLLASVHQLQ-----GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND-----IASKPSQEHIFKVED- 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
              PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Signal; Magnesium; Calcium; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 143.5; DB 1; Length 1163;
24.8%; Pred. No. 0.00065;
Live 43; Mismatches 89; Indels 35;
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                                                                                                                       CYTOPLASMIC (POTENTIAL)
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FG-GAP 4.
FG-GAP 5.
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FG-GAP 7.
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FG-GAP 2.
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
                                                                                                                                                                                                                                     MEDLINE-92011862: Pubbled-1918137;
Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,
Nishida Y., Obara M., Kimata K.;
The complete primary structure of type XII collagen shows a chimeric
molecule with reliterated fibronectin type III motifs, von Willebrand
factor A motifs, a domain homologous to a noncollagenous region of
type IX collagen, and short collagenous domains with an Arg-Gly-Asp
site.;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=95370352; PubMed=7642694;

Roch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;

"Large and small splice variants of collagen XII: differential
expression and ligand binding.";

J. Cell Biol. 130:1005-1014(1995).

-!- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBRILS, AND THE COLL DOMAINS MAY BE
LOCALIZED IN THE PERIFIBRILLAR MATRIX.
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DOMAIN: THIS SEQUENCE DEFINES FIVE DISTINCT DOMAINS, TWO TRIPLE-HELICAL DOMAINS (COL1 AND COL2) AND THREE NONTRIPLE-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (Ca-x-Y) ARE HYDROXYLAFED IN SOME OR ALLO OF THE CHAINS. PTM: GLYCOSYLATED. CHONDROITIN-SULFATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERMOPTED HELICES (FACIT) FAMILIX.
SIMILARITY: CONTAINS 4 VWFA DOMALIX.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-1283 FROM N.A. (SHORT FORM), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.; "Type XII collagen. A large multidomain molecule with partial homology to type IX collagen "; 5 Biol. Chem. 264:19772-19778[1989].
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PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2960-3076 FROM N.A., MEDLINE-87317590; PUDMEd-3476325. GOXDOM M.K., GETECKE D.R., Olsen B.R.; "Type XII collagen: distinct extracellular matrix component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discovered by cDNA cloning.";
Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
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MEDLINE=90062079; PubMed=2584192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Cell Biol. 115:209-221(1991).
                                                                                                                                                                                                                        STRAIN-WHITE LEGHORN;
                                                                                                                                                                     SEQUENCE FROM N.A
                                                                              NCBI_TaxID=9031;
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                                                                                                                                                                                            DR EMBL; M17375; AAA4807011.; -
DR EMBL; M17375; AAA480781.; -
DR EMBL; M17376; A28037; A28037.
DR EMBL; M17376; AA4485.
DR PIR; A34485; A34485.
DR PIR; A34485; A34485.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FN_III.
DR InterPro; IPR003962; FN_III.
DR InterPro; IPR003962; FN_III.
DR InterPro; IPR003129; TSPN.
DR Pfam; PF021391; Collagen; 4.
DR Pfam; PF020210; TSPN; 1.
DR Pfam; PF00092; VWFA.
DR Pfam; PF00092; VWFA.
DR PRINTS; PR000014; FNYTPEII.
DR PRINTS; PR00014; FNYTPEII.
DR SWART; SW00050; TSPN; 1.
DR SWART; SW00127; VWA; 4.
DR SWART; SW00327; VWA; 4.
DR SWART; SW00127; VWA; 4
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WITH 1 IMPERFECTION.
NONHELLCAL REGION (NC2).
TRIPLE-HELLCAL REGION (COL1)
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FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 17.
FIBRONECTIN TYPE-III 18.
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NONHELICAL REGION (NC1).
ASP/GLU-RICH (ACIDIC).
ARG/LXS-RICH (BASIC).
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 11, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
EMBO J. 7:1371-1378(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                               215 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP 271
                                                                                                                                                                                                                                                                                                                44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
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STRAIN-BALB/C; TISSUB-Spleen;
MEDLINE-86287312; PubMed-2942940;
MEDLINE-86287312; PubMed-2942940;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
"A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
N-LINKED (GLCNAC. ..) (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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N-SING (IN SHORT ISOFORM).
T -> S (IN REF. 4).
D -> E (IN REF. 2).
L -> F (IN REF. 2).
U -> F (IN REF. 2).
U -> F (IN REF. 2).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                            8.3%; Score 143; DB 1; Length 3124; 26.1%; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                          97; Indels
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094285AFE7F346CF CRC64;
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Best Local Similarity 2000.
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                                                          Springer T.A., Teplow D.B., Dreyer W.J.;

Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion

"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion

"Sequence homology of the LFA-1 and Mac-1

"In Sequence homology of the LFA-1

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                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-i- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-i- SIMILARITY: CONTAINS I VWFA DOMAIN.
-i- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                                                                                                                                                                                                                                                                                                                                                      ASSOCIATES WITH BETA-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
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PRINTS; PR0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS0234; VWFA; 1.
Integrin; Call adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Calcium; Repeat.
                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M
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 Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986)
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
POTENTIAL.
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FG-GAP 2.
VWFA.
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HSSP; P11215; 1A8X.
MGD; MGI:96607; Itgam.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; Integrin_A; 1.
                                              MEDLINE-85188276; PubMed-3887182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.2%; Score 141; DB 1; Length 1153;
Best Local Similarity 24.2%; Pred. No. 0.001;
Matches 71; Conservative 50; Mismatches 96; Indels 76; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 98
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STRAIN=SWISS WEBSTER, AND C57BL/6J; TISSUE=Skin;
MEDLINE=96170761, PubMed=8601036;
Boohme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-MRR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain precursor.
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RE Gevelopment.";

Dev. Dyn. 204:432-445(1995).

EL Dev. Dyn. 204:432-445(1995).

COTATAINON: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-

CONTAINING FIBRILS, THE COLI DOMAIN COULD BE ASSOCIATED WITH THE

CONTAINING FIBRILS. AND THE COLZ AND NG3 DOMAINS MAY BE

SURFACE OF THE FIBRILLAR MATRIX (BY SIMILARITY).

COCALAGEN THE PERIFIBRILLAR MATRIX (BY SIMILARITY).

CONTAINING 190 kDa OF

NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).

CONTAINING 190 kDa OF

COLLAGEN XII MAY CONTAIN HOMOTRIMER OF EITHER THE LONGER

FORM OF COLLAGEN XII MAY COMBINATIVE SPLICING. THE FINAL TISSUE

SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE

SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE

COR THE SHORTER ISOPORM OR ANY COMBINATION OF LONG AND SHORT

CORNER, SCLERA, BLODD VESSELS, AND PERIOSCHIVAN.

CONNER, SCLERA, BLODD VESSELS, AND PERIOSCHOUDRIUM,

CONNER, SCLERA, BLODD VESSELS, AND PERIOSCHOUN XII, XIIA, IS THE

PREDOMINANT FORM AT EARLY STAGES (ED7 AND 11); AT LATER STAGES OF

FORM, AS THE SHORT FORM BENDESSED IN SEVERAL TISSUES, EVEN AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                                                                                                                                                                                   -i- PTM: GLYCÓSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
-i- SIMILARITY: CONTAINS 4 WOFF DOMAINS.
-i- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLAGEN ALPHA 1(XII) CHAIN FIBRONECTIN TYPE-III 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIBRONECTIN TYPE-III 3. FIBRONECTIN TYPE-III 4. FIBRONECTIN TYPE-III 5. FIBRONECTIN TYPE-III 5. FIBRONECTIN TYPE-III 7. FIBRONECTIN TYPE-III 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:88448; Coll2al.
InterPro; IPR000087; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FN_III.
InterPro; IPR003129; TSPN.
InterPro; IPR003129; TSPN.
InterPro; IPR002035; VWFA.
Pfam; PF00191; Collagen; 4.
Pfam; PF001041; fn3; 18.
Pfam; PF00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWFA 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U25652; AAA99719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00453; VWFADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00060; FN3; 16
SMART; SM00210; TSPN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3067
114
316
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101 QIRQGLEELQKVL----PGGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 153
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TO CHONDROITH SULFATE (POTENTIAL).
TO CHONDROITH SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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HYDROXYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                  NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
                                                                                                                                                                                                                                                                                                     NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.
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                                                         FIBRONECTIN TYPE-III
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                                                                                                                                                                                                                           VWFA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 IHSILKKSCIEI---LAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613 SFVLTQSICLRIEQELAA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   893
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868
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Best Local Similarity
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2533
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1388
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12;

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PROSITE; PSS0240; TRYPSIN_DOM: 1.
PROSITE; PS00134; TRYPSIN_HIS: 1.
PROSITE; PS00135; TRYPSIN_SER: 1.
PROSITE; PS50234; VWFA: 1.
Complement pathway: Plasma: Glycoprotein; Hydrolase; Serine protease; Signal; Repeat; Sushi; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-------NRQGYRTAS- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| | : : : | : : | :: | :: ERSQ------DVTEVITSLESASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----KD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :|| :|| || || GHLNLYLLLDASQSVTEKDFIDFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE 97
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.004;
56; Mismatches 115; Indels
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D7DE9DEF4DBA48D9 CRC64;
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C2B FRAGMENT.
C2A FRAGMENT.
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SUSHI 2.
SUSHI 3.
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InterPro; IPR001314; Sushi_SCR_CCP.
InterPro; IPR001245; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR001255; vWFA.
Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PF00092; vwa; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00032; CCP; 2.
SWART; SW00032; CCP; 2.
  EMBL; M60577; AAA37381.1; JOINED.
EMBL; M60578; AAA37381.1; JOINED.
EMBL; M57891; AAA3294.1; -.
PIR; A38876; C2MS.
HSSP; P00757; ISGF.
MEROPS; S01.194; -.
MGD; MGI:88226; C2.
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606
760 AA;
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CHAIN 19
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251
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                                                                                                                                                                                                                                                                                                         IShikawa N., Nonaka M., Wetel R.A., Colten H.R.;

"Murine complement C2 and factor B genomic and cDNA cloning reveals
different mechanisms for multiple transcripts of C2 and B.";
J. Biol. Chem. 265:19040-19046(1990).

-I- FUNCTION: COMPONENT C2 WHICH IS PART OF THE CLASSICAL PATHWAY OF
THE COMPLEMENT SYSTEM IS CLEAVED BY ACTIVATED FACTOR C1 INTO TWO
THE COMPLEMENT FACTOR 4B TO GENEVATE THE C3 OR C5 CONVERTASE.

-I- CATALYTIC ACTIVITY: CLEAVES C3 IN THE ALPHA-CHAIN TO YIELD C3A AND
C13B. CLEAVES C5 IN THE ALPHA-CHAIN TO YIELD C3A AND C5E. BOTH
CLEAVEGES TAKE PLACE AT THE C-TERNING OF AN AGININE RESIDUE.

-I- MISCELLANBOUS: C2 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
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-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) DOMAINS.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
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                                                                                                                                                                                                                                                                                                                                                                               Genomics 41:236-242(1997).

Genomics 41:236-242(1997).

1- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIRELS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SUBRACCE OF THE FIRERILAR MATRIX (92 SIMILARITY).

1- SUBUNIT: TRIMER OF IDENTICAL REQUENCES.

NOWTRIPEL-HELICAL SEQUENCES.

1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING; THE FINAL TISSUE
FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIBERS OF EITHER THE LONGER
OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT
ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROPEGLICAN.

1- TISSUE SPECIFICITY: FOUND IN COLLAGEN I-CONTAINING TISSUES: BOTH
SHORT AND LONG ISOFORMS APPERR IN AMMION, CHORION, SKELETAL
MUSCLE, SMALL INTESTINE, AND IN CELL CULTURE OF DERMAL
HUSCLES, KERATINOCYTES, AND ENDOTHELIAL CELLS. ONLY THE SHORT
ISOFORM IS FOUND IN LUNG, PLACEBTA, AND A SQUAMOUS CELL
ISOFORM IS FOUND IN LUNG, PLACEBTA, AND A SQUAMOUS CELL
ISOFORM IS FOUND IN LUNG, PLACEBTA, AND A SQUAMOUS CELL
CANCINGMA CELL LINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                243 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 298
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).
MEDLINE-9728851; PubMed-914499;
Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.;
and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(XI)
collagen (COL9A1), and alpha 1(XIX) collagen (COL12A1), alpha 1(XIX)
Genomics 41:236-243.";
Genomics 41:236-242(1997).
                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
PTM: GLYCOSYLATED, CHONDROITIN-SULFATED COLLAGENS WITH
SIMILARITY: BELONGS TO THE FIBRIL. ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: CONTAINS 4 VWFA DOMAINS.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                           CAIC_HUMAN STANDARD; PRT; 3063 AA. 099715; 099716; 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) collagen alpha 1(XII) chain precursor. COL12A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U73778; AAC51244.1; -.
EMBL, U73779; AAD40483.1; -.
HSSP; P02751; ITTE.
                                                                                      531 VGDPTSQHGKEFLVEDVII 549
                                                                 299 MND-----GLSFISSSVII 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U73779; A.
HSSP; P02751; 1:
MIM; 120320; -.
                                                                                                                                      CA1C_HUMAN
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PROSITE; PS50234; VWFA; 4. Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing. SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WATTH I TANGEDINON (NC2).

TRIPLE-HELICAL REGION (NC1).

WITH 2 IMPERETORION (COL1)

WITH 2 IMPERETORIONS.

NOMHELICAL REGION (NC1).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

HYDROXYLATION (BY SIMILARITY).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLAGEN ALPHA 1(XII) CHAIN. FIBRONECTIN TYPE-III 1.
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FIBRONECTIN TYPE-III 2.
VWFA 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
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FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 17
FIBRONECTIN TYPE-III 16
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FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
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FIBRONECTIN TYPE-III
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Interpro; IPR003961; FN III.
Interpro; IPR003962; FNIII_repeat.
Interpro; IPR003129; TSPN.
Interpro; IPR02035; VWFA.
                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0014; PNTYPEIII.
PRINTS; PRO0453; VWFADDMAIN.
SMART; SMO0060; FN3, 17.
SMART; SMO010; TSPN; 1.
                                                                                                                                                                                    Pfam; PF01391; Collagen; 4. Pfam; PF00041; fn3; 18. Pfam; PF02210; TSPN; 1. Pfam; PF00092; vwa: 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                     98 DREQIRGGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 153
                                                                                                                                      154 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI 211
                                                   Gaps
                                                                   44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Extracellular matrix.

TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION; HIGH PRESENCE IN DENSE CONNECTIVE TISSUE IN SKELETAL MUSCLE.

PTW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                Waelchli C., Trueb J., Kessler B., Winterhalter K.H., Trueb B.; "Complete primary structure of chicken collagen XIV."; Eur. J. Biochem. 212:483-490(1993).
                                                   26;
                                  Score 131; DB 1; Length 3063;
                                                   75; Indels
MISSING (IN SHORT ISOFORM).
W; 75FEA78FA8E48293 CRC64;
                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XIV) chain precursor (Undulin).
                                        Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                       undulin.";
                                                                                                                                                                                                                                      PRT; 1888 AA
                                                  38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 402-1549 FROM N.A. MEDLINE-92339443; PubMed=1339349; Trueb D., Trueb B.; a variant of Type XIV collagen is a variant of Eur. J. Blochem. 207:549-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99280705; Pubmed-10350466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMOTRIMER (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryo;
MEDLINE=93185668; PubMed=8444186;
        333189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
STRUCTURE BY NMR OF 1852-1885.
                                 7.6%;
                                                                                                                                                                          212 IHSILKKSCIEI---LAA 226
                                                                                                                                                                                         609 SFELTOSICLRIEGELAA 626
                                                   59; Conservative
                                                                                                                                                                                                                                      STANDARD;
25 1180
3063 AA;
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTORS.
                                                                                                                                                                                                                                    CA1E_CHICK
P32018;
VARSPLIC
SEQUENCE
                                 Query Match
                                            Best Local
                                                                                                                                                                                                                                                                                        COL14A1
                                                                                                                                                                                                                                                                                                                          Gallus
                                                                                                                                                                                                                             CA1E_CHICK
                                                  Matches
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LYSINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00453; v....
PRINTS; PR00463; v....
SMART; SM00200; TSPN; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00210; VWFA; 2.
PROSITE; PS50234; VWFA; 2.
PROSITE: PS50234; VWFA; 2.
PROSITE: PS50234; VWFA; 2.
PROSITE: PS50234; VWFA; 2.
PROSITE: PS50234; VWFA; 2.
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PROSITE: PS50234; VWFA; VWFA; 2.
PROSITE: PS50234; VWFA; VW
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                               UNIT ARE HYDROXYLATED IN ALL CASES AND BIND CARBOHYDRATE.
PTM: MAY CONTAIN CYSTEINE RESIDUES INVOLVED IN INTER- AND
INTRAMOLECULAR DISULFIDE BONDING.
SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: CONTAINS 2 VWEA DOMAINS.
SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
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CELL ATTACHNENT SITE (POTENTIAL).
CELL ATTACHNENT SITE (POTENTIAL).
WW. 39915BB9F46DB973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 130; DB 1; Length 1888; 25.0%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NONHELICAL REGION (NC4).
TRIPLE-HELICAL REGION 1.
TRIPLE-HELICAL REGION 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB: 1899; 25-FEB-99.
PDB: 1890; 25-FEB-99.
InterPro: 187000087; Collagen.
InterPro: 187000087; Collagen.
InterPro: 18700087; FNIII_repeat.
InterPro: 187002035; VWFA.
InterPro: 187002035; VWFA.
Pfam; PF001391; Collagen; 4.
Pfam; PF00041; fn3; 8.
Pfam; PF000921; VWs: 2.
PRINTS: PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X70793; CAA50064.1; -. EMBL; X70792; CAA50063.1; -. EMBL; X66138; CAA46928.1; -. PIR; S22916; S22916.
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                              1213 DELITFVCETASATCPLVFKDGDKLA-----GFKMMENFGLVEKEFSAIDGVSMEPGTF 1266
            156 DLFFYSEREANRSRDL-GALVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 212
                                                                               272
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                               213 HSILKKSCIEILAAEPSTICAGESFOVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF
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                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
17-CCT-2001 (Rel. 40, Last annotation update)
17-CCT-2001 (Rel. 40, Last annotation update)
17-CCT-2005 3 in chromosome III (Fragment).
17-CCT-2005 3.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
GGF-LIKE 1 (PARTIAL).
EGF-LIKE 3.
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PS00022; EGF_1; 1.
PS01186; EGF_2; 5.
PS01187; EGF_CA; 1.
PS50024; SEA; 2.
PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 230423; CAA83007.1; -.
PIR; $42373; $42373.
HSSP; P02468; 1TLE.
WOTMPEP; T20G5; 31; CED0478.
INTERPO; IPR000152; ASX_hydroxyl.
INTERPO; IPR001561; EGF-like.
INTERPO; IPR001881; EGR-Ca.
INTERPO; IPR001881; EGR-Ca.
INTERPO; IPR001881; EGR-Ca.
INTERPO; IPR001881; EGR-Ca.
INTERPO; IPR001891; EGR-Ca.
Ffam; PF001390; SEA: 2.
Pfam; PF001390; SEA: 2.
Pfam; PF001390; SEA: 2.
SMART; SM00179; EGF_CA: 1.
SMART; SM00179; EGF_LIKe; 38.
SMART; SM00200; SEA: 2.
SMART; SM00200; SEA: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00022; EGF_1; PROSITE; PS01186; EGF_2; PROSITE; PS50024; EEF_2 PROSITE; PS50024; WWFA; Hypothetical protein; EC NON_TER 1 1 DOMAIN 1 2701 TRANSMEM 2702 2722
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                                                                                                                                                         273 SVEDTYLL 280
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P34576;
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                                          121
                                                          601
                                                                           --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-91060558; Pubmed-2246248;
MEDLINE-91.060558; Pubmed-2246248;
Medrins R.N., Obborne-Lawrence S.L., Sinclair A.K., Eddy R.L. Jr.,
Byers M.G., Shows T.B., Duby A.D.;
"Structure and chromosomal location of the human gene encoding
                                                                                                                                                                                                                                                                                                                        cartilage matrix protein.";
J. Biol. "Chem. 265:19624-19631(1990).
-!- FUNCTION: CARTILAGE MATRIX PROTEIN IS A MAJOR COMPONENT OF THE EXTRACELLULAR MATRIX OF NONARTICULAR CARTILAGE. IT BINDS TO
         ---- DLYFILDKSGSVLHH--WNEIYYFVEQLA
                  602 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN
                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                           71 HKFI--SPOLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                              175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
                                                                                                                       649 TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS 697
                                                                                                                                                                                        01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cartilage matrix protein precursor (Matrilln-1).
MATNI OR CRIM OR CMP.
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EMBL, M55675; AAB38702.1; JOINED.
EMBL, M55677; AAB38702.1; JOINED.
EMBL, M55677; AAB38702.1; JOINED.
EMBL, M55689; AAB38702.1; JOINED.
EMBL, M55681; AAB38702.1; JOINED.
EMBL, M55681; AAB38702.1; JOINED.
EMBL, M55681; AAA63904.1; JOINED.
EMBL, M55681; AAA63904.1; ALT_SEQ.
PIR, A37979; A37979.
HSSP, P05099; 1AQ5.
MIN: 114437; -.
InterPro: IPR002055; WGFA.
Pfam; PF00008; Way; 2.
Pfam; PF00092; Way; 2.
Pfam; PF00092; Way; 2.
Pfam; PR00181; EGF; 1.
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF, 1.
SMART; SM00181; EGF_1.
                                                                                                                                                                                                                               Homo sapiens (Human).

Eukaryota; Metazoa; Chordata;

Mammalia; Eutheria; Primates;

NCBI_TaxID=9606;
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SUBUNIT: HOMOTRIMER.
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P21941;
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929 AA;
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57; Conserv
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A DEVELOPMENTAL ROLE IN REGENERATION.
SUBUNIT: TRIMER OF IDENTICAL CHAINE BACH CONTAINING 190 KDB OF NONTRIPEL-HELICAL SEQUENCES (BY SIMILARITY).
DEVELOPMENTAL STAGE: EXPRESSION STARTS AT 3 DAYS AFTER AMPUTATION IN CELLS OF THE BASAL LAYER OF THE WOUND EPITHELIUM, AT DAY 10, IN CELLS OF THE BASAL LAYER OF THE WOUND EPITHELIUM, A DAY 10, THE DISTAL MESENCHYME CELLS. AT MID-BUD AND LATE-BUD BLASTEMA STAGES, WOUND EPITHELIUM EXPRESSION HAS DECREASED, WHEREAS THE MESENCHYME STAGEN ACTIVE IN TRANSCRIPTION AND SHOWED A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 ENROGYRTAS--VIIALIDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
                    Signal; Glycoprotein; Cartilage; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                 82 FIV---FSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y 133
                                                                                                                                                                                                                                                                                    315 GLVQYSSSVRQEFPLGRFHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSF 366
                                                                                                                                                                                                                                            264 VCSGGGGS-----SATDLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQV 314
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                          24 ICAGQGGRREDGGPACYGGFDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMS 81
                                                                                                                                                                                                                                                                                                                                                ADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 243
                                                                                                                                                                                                                                                                                                                                                           | SEPVAEHYEYTAD-FKTINQIGKKLQKKICVE---EDP---CACESLVKFQAKVEG 472
                                                                                                                                                                                                                                                                                                                             TVSSGARPGAQKVGIVFTDGRSQD----YINDAAKKAKDLGFKMFAVGVGNAVEDELREI
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
collagen alpha (IXII) chain (Fragment).
Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                           . .) (POTENTIAL).
                                                                                                                                                                                                        45;
                                                                                                                                                                                    Length 496;
                                                                                                                                                                                                         Indels
                                                                                                                                                         2D880A8114C7940F CRC64;
                                            CARTILAGE MATRIX PROTEIN.
                                                                                COILED COIL (POTENTIAL).
N-LINKED (GLCNAC. . . ) (
POTENTIAL.
                                                                                                                                                                                      DB 1;
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                                                                                                                 SIMILARITY. SIMILARITY.
                                                                                                                                                                                                           37; Mismatches
                                                                                                                BY SIMILAR
BY SIMILAR
BY SIMILAR
POTENTIAL.
                                                       VWFA 1.
EGF-LIKE.
VWFA 2.
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      EGF_2; 1.
VWFA; 2.
                                                                                                                                                           53700
                                                                                                                                                                                                             Conservative
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                                      22
496
222
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496 AA;
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                                                                                                                                                                                                  Similarity
       PS01186; 1 PS50234; 1
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                              EGF-like domain;
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Best Local Simi
Matches 60;
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Q91145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 102
                                                  693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIALLLTDGKSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI
TENDENCY TOWARD DISTAL REGIONALIZATION. CONDENSING CARTILAGE SHC
NO SIGNAL. FINALLY, AT THE LATE DIGIT STAGE, EXPRESSION BECOMES
LARGELY RESTRICTED TO THE PERICHONDRIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50234; VWFA; 2.
Extracellular matrix; Connective tissue; Repeat; Cell adhesion;
                                                                                                                        DB 1; Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
VWFA 2.
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FIBRONECTIN TYPE-III 8.
TO CHONDROITIN SULFATE (F
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N-LINKED (GLCNAC. . . ) (F
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21.2%; Pred. No. 0.061;
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FIBRONECTIN 7
FIBRONECTIN 7
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InterPro; IPR003961; FN_III.
InterPro; IPR002035; vWFA.
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SMART; SM00327; VWA; 1.
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Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collagen; Glycoprotein
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:44:32; Search time 507.33 Seconds Run on:

(without alignments)
151.246 Million cell updates/sec

1131 1 MSFIVFSTRGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT 218 US-09-970-076-10

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

3502263 seqs, 351980561 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodate/2/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodate/2/paa/USO6_COMB.pep:*

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26: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

26: /cgn2_6/ptodate/2/paa/USO9_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 10, Appl Sequence 2121, Ap Sequence 50, Appl Sequence 132, App Sequence 132, App Sequence 33, App Sequence 34, Appl Description alcho US-09-970-076-10 US-09-488-725A-2121 PCT-US99-31025-50 3 US-09-471-179-50 PCT-US99-31025-132 3 US-09-471-179-50 PCT-US99-31025-30 Match Length DB 100.0 Query Result

Sequence 51, Appl Sequence 30, Appl	Sequence 51, Appl	Sequence 9,	6 9	σ	Ñ	8, A		94,	quence 621, A	e 621,	187	equence 232,	9	25,	620, A	620,	194,	301,	105, 7	e 105	1574	1574,	27, A	Sequence 27,	26, A	26,	107,	ĭ	'n	57	59,	61	e 2,	Sequence 57, Appl	•
1 PCT-US99-31025-51 18 US-09-471-179-30	18 US-09-471-179-51 1 PCT-11500-31025-0	16 US-09-223-546-9	18 US-09-471-179-9	19 US-09-599-596-9	21 US-09-796-753-12	23 US-09-970-076-8	23 US-09-970-076-2	1 PCT-US00-30045-94	1 PCT-US01-11988-621	22 US-09-833-245-621	23 US-09-918-715-187	23 US-09-918-715-232	23 US-09-970-076-6	1 PCT-US00-30045-125	1 PCT-US01-11988-620	22 US-09-833-245-620	23 US-09-918-715-194	3 US-09-91	PCT-US99-3	9-471-179-1	450-157	S01-16450A	226-2	745-2	226	745-2	05226-1	6-74	.05226-	05226-5	5226-	PCT-US00-05226-	US-09-516-745-		
306	306	333	333	333	333	333	368	403	403	403	564	564	564	403	403	403	262	295	172	172	272	272	284	284	455	455	487	487	488	488	488	488	488	488	488
85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	5.	ď.	δ.	5.	4	•	Ξ.	61.8	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7
996	996	996	996	996	996	996	996	996	996	996	996	996	996	961	961	961	960	960	669	669	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206
ထတ	10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

APPLICANT: Young, John A.T.
APPLICANT: Bradley, Renneth A.
APPLICANT: Bradley, Renneth A.
APPLICANT: Bradley, Renneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 96026.9745
CURRENT PELLOATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1 Sequence 10, Application US/09970076 GENERAL INFORMATION: ; ORGANISM: Homo sapiens US-09-970-076-10 01-920-016-60-SD SEQ ID NO 10 LENGTH: 218 PRT

Gaps ö DB 23; Length 218; Indels Score 1131; DB 23; Pred. No. 4.5e-112; Ouery Match
100.0%; Score 1131;
Best Local Similarity 100.0%; Pred. No. 4.5
Matches 218; Conservative 0; Mismatches

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Gaps

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RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application US/09471179
Sequence 50, Application US/09471179
Sequence 50, Application:
Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REPERENCE: 7853-173
CURRENT PILING DATE: 1999-12-23
PRIOR PELLOR DATE: 1999-12-30
PRIOR FILING DATE: 1998-12-30
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                                                                                                                                                                                                                                                                                                           Score 966; DB 1; Length 274;
Pred. No. 2.9e-94;
2; Mismatches 0; Indels
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APPLICANT: Millennium Pharmaceticals, Inc.; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS FILE REFERENCE: 7853-173-228 CURRENT APPLICATION NUMBER: PCT/US99/31025 CURRENT FILING DATE: 1999-12-23 EARLIER APPLICATION NUMBER: 09/223,546 EARLIER PILING DATE: 1999-12-30 NUMBER OF SEQ ID NOS: 135 SOUTHARD: FASTESEQ for Windows Version 4.0 SEQ ID NO 50 LENGTH: 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.4%; Score 966; DB 18;
Best Local Similarity 98.9%; Pred. No. 2.9e-94;
Matches 188; Conservative 2; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                 Query Match 85.4%;
Best Local Similarity 98.9%;
Matches 188; Conservative
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US-09-471-179-50
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PCT-US99-31025-50
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233 KINDSVTLNE 242
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US-09-471-179-50
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LENGTH: 274
                                                                                                                                                                                                                                 TYPE: PRT
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                                    PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF
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APPLICANT: Hyseq Inc.

TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

FILE REFERENCE: 784FLPGT

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US/09/488,725

PRIOR APPLICATION NUMBER: US09/552,317

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US09/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-09-31

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-10-19

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 7144

SECTIVARE: PLE-L-Genes_D Versions 1.0

LENGTH: 298
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PCT-US99-31025-50

) Sequence 50, Application PC/TUS9931025

, GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 218; Conservative
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US-09-488-725A-2121
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121 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
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                                                                                        RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REPERENCE: 7853-173-228
CURRENT ELLING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: 09/223,546
SERLIER APPLICATION NUMBER: 09/223,546
SERLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 30
LENGTHR: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 30, Application PC/TUS9931025 ; GENERAL INFORMATION:
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98.9%;
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PCT-US99-31025-30
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Best Local Similarity
Matches 188; Conserv
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PCT-US99-31025-30
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PCT-US99-31025-51
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GENERAL INFORMATION:
APPLICANT: Holtzman. Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT APPLICATION NUMBER: 09/223,546
EARLIER APPLICATION NUMBER: 09/223,546
SARLIER APPLICATION NUMBER: 09/223,546
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Pred. No. 3.3e-94;
2; Mismatches 0
                                                                                                                                                                                                                                             Sequence 132, Application PC/TUS9931025 GENERAL INFORMATION:
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98.98;
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Best Local Similarity 98.99
Matches 188; Conservative
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; ORGANISM: Homo sapiens
US-09-471-179-132
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PCT-US99-31025-132
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260 KINDSVTLNE 269
                                  181 KINDSVTLSK 190
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ENGTH: 301
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RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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  Length 306;
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceticals, Inc.
TITLE OF INVENTION: SCRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-173-228
CURRENT PAPLICATION NUMBER: PCT/US99/31025
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: 09/223,546
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
                                                0; Indels
Score 966; DB 1;
Pred. No. 3.4e-94;
2; Mismatches 0
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RESULT 11
PCT-US99-31025-9
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                                                                                                                                                                                                                   Gaps
                                                                                                                      Sequence 30, Application US/09471179
Sequence 30, Application US/09471179
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REPERBNCE: 7853-173
CURRENT FILING DATE: 1999-12-23
RIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/223,546
PROR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 306
                                                                                                       1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                 Gaps
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Pred. No. 3.4e-94;
2; Mismatches 0;
                                                          Score 966; DB 1; L
Pred. No. 3.4e-94;
2; Mismatches 0;
                                                                                    2; Mismatches
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GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
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Best Local Similarity 98.9%;
Matches 188; Conservative
                                                           85.4%;
ilarity 98.9%;
Conservative
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 188; Conserv
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                        PCT-US99-31025-51
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US-09-471-179-30
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61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM FILE REFERENCE: 7853-173
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sequence 9 Application PC/TUS9931025
sequence INFORMATION:
APPLICANT: Millennium Pharmaceticals, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: 09/223,546
EARLIER APPLICATION NUMBER: 09/223,546
SEALIER PLING DATE: 1998-12-30
NUMBER OF SEQ. ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.8e-94;
2; Mismatches 0;
                                                                                                                                                                                                                                                          Score 966; DB 18;
Pred. No. 3.4e-94;
2; Mismatches 0;
                                CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1988-12-30
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 51
LENGTH: 306
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98.9%;
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milarity 98.9%;
Conservative 2
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Best Local Similarity 98.9
Matches 188; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-09-471-179-51
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61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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Sequence 9, Application US/09599596
GENERAL INFORMATION:
Sequence 9, Application US/09599596
GENERAL INFORMATION:
PAPLICANT: HOLYZMATION:
DOUGLES BECREBED FOTEINS AND NUCLEIC ACIDS ENCODING THEM FILE OF INVENTION: SECREBED PROTEINS AND NUCLEIC ACIDS ENCODING THEM FILE REFERENCE: 09404/06601
CURRENT FILING DATE: 2000-06-22
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRALEEQ FOR WINDOWS Version 3.0
SEQ ID NO 9
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1 Sequence 12, Application US/09796753

2 Sequence 12, Application US/09796753

3 GENERAL INFORMATION:

3 APPLICANT: MCDRATION:

5 TILLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

5 FILE REFERENCE: 7853-227-999

5 CURRENT APPLICATION NUMBER: 09/183,175

6 PRIOR APPLICATION NUMBER: 09/183,175

7 PRIOR PILING DATE: 1998-10-30

7 PRIOR PILING DATE: 1998-10-30

7 PRIOR FILING DATE: 1998-12-30

7 PRIOR FILING DATE: 1998-10-2-26

7 PRIOR PILING DATE: 1998-10-2-26
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Pred. No. 3.8e-94;
2; Mismatches 0;
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Best Local Similarity 98.9%;
Matches 188; Conservative
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GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: HOLIZMAN. DOUGLED
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 09/223,546
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                               APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 0940/4066001
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
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                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                              Sequence 9, Application US/09223546 GENERAL INFORMATION:
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Matches 188; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-09-223-546-9
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260 KINDSVTLNE 269
  181 KINDSVTLSK 190
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260 KINDSVTLNE 269
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Best Local Simi
Matches 188;
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US-09-471-179-9
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TYPE: PRT
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PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-29
PRIOR PRIOR PRIOR NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-20
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
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PRIOR FILING DATE: 1999-12-29
PRIOR PRIOR PRIOR NUMBER: 09/474,071
PRIOR PRILING DATE: 1999-12-29
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/550,7993
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/559,596
PRIOR FILING DATE: 2000-06-22
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CORGANISM: Homo sapiens
US-09-796-753-12
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AL542724 LTI_FL002_PL1 Homo sapiens cDNA clone CSODE011YL09 5 prime, mRNA sequence.
AL542724 AL1_AL1002_PL1 Homo sapiens cDNA clone CSODE011YL09 5 prime AL542724
AL542724 GI:12875049
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 1063)

Li,W.B., Gruber,C., Jossee,J. and Polayes,D.

Full-length cubra, C., Jossee,J. and normalization

Unpublished (2001)

Contact: Genoscope.

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr.
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BE146205
BB649806
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AV667876
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Manmalia; Sutheria; Primates; Catarrinii; Hominidae; Homo.

Manmalia; Sutheria; Primates; Catarrinii; Hominidae; Homo.

RS NIH-WGC http://mgc.nci.nih.gov/.

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomistribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Lond distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Loration/Qualifiers

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                                 Craniata; Vertebrata; I
Catarrhini; Hominidae;
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Pred. No. 5.8e-93;
0; Mismatches 29;
                                     Chordata;
                                                                       Primates;
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Best Local Similarity 95.4%;
Matches 839; Conservative
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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BG281561 820 bp mRNA linear EST 21-FEB-2001 602402412F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544691 5',
the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." 17 c 292 g 193 t
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                                                                                                                                            1 aggacccgcgaggaagggcccgcggatggcgcgcctgagggtcgtggcgagttcgcgg
                                                                                       Length 963
                                                                                                                 Indels
                                                                                     Ouery Match

48.7%; Score 688; DB 10;
Best Local Similarity 96.8%; Pred. No. 9.6e-86;
Matches 724; Conservative 0; Mismatches 20;
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NH-MGC http://mgc.nci.ndi.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue procurement: DorDvDTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

CONTROL CONSORTIUM/LLNL at:

High quality sequence stop: 718.

Location/Oualifiers

Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                963 bp mRNA linear EST 27-FEB-2001 G02425082F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4563020 5', mRNA Sequence.
BG326444
BG326444.1 GI:13132881
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                         480
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Mammalia; Eutheria;
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/organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone='Insage:454469"
/clone=lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab.host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTBT; Site_1: XhoI; Site_2: BcoRI; ONA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (SIratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 820)

I (bases 1 to 820)

INIH-MGC http://mgc.nci.nih.gov/.

INIH-MGC http://mgc.nci.nih.gov/.

I Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Preparation: Ling Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence stop: 815.

Location/Qualifiers

Location/Qualifiers
               Euteleostomi;
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); Mismatches 19; Indels
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ORIGIN
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linear HTC 19-JAN-2002
CDNA, RIKEN full-length
to CDNA FLJ10601 FIS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                 655
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HTC: CARP trapper.
Mus musculus (strain:C57BL/6J) 10, 11 days embryo CDNA tolone_lib:RIKEN full-length enriched mouse CDNA library
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Functional annotation of a full-length mouse cDNA
Nature 409, 685-690 (2001)
S (bases i to 1614)
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Aral, A., Arawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Koşukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koşukawa, T., Kurihara, C., Matesuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sahai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, T., Taya, Y., Toya, T., Yamanura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flease visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAAGAAAGATCAAGAGCTTTTTTTTTTTTTTTTTYN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5.
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GLPKKKWPTVDASYYGGRGVGGIRNEVRGEKGSTEEGAKLEKAKARAKVKNFDGEYE
FPEPRNLANNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTFFRGWR
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....forganism="Mus musculus"

/strain="C57BL/6J"

/db_xref="MGD:MG1:1904936"

/db_xref="taxon:10090"

/clone="2810405N18"

/clone=lib="RIRBN full-length enriched mouse cDNA library"

/dev_stage="10, 11 days embryo"
                                                                                                                                                                                                                                                                                                                                            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, Pax:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mkLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENS
QGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="data source:SPTR, source key:Q9NVP3, evidence:ISS homolog to CDNA FLJ10601 FIS, CLONE NT2RP2005000
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Pred. No. 6.4e-85;
0; Mismatches 91; Indels 0;
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EST 15-SEP-2000
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE741333 725 bp mRNA linear EST 15-SEP-2
601594179Fl NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3948114 5',
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                                                                                                                                                                                                                                                                                                     242 GACCITGGIGCGAITGITIACIGCGIIGGCGIGAAGGAITICAAIGAAACICAGIIGGCI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                      ggcatcatccactcaattttgaagaagtcctgcatcgaaattctagcagctgaaccatcc
                                                                                                                                                                                                                                                                                                                                                                       gtcatcatcaccaccacacatgttctgacggttccatcctggccatcgcctgctgatc
                                                                       gatcttggtgcaattgtttactgtgttggtgtgaaagatttcaatgagacacagctggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1151 attatcaaggaggtccctccacccctgccgaggagagtgaggaaaa 1197
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BE741333.1 GI:10155325
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AUTHORS
TITLE
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/issue__ippe="melanotic melanoma"
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/nab_host="DHIOB (phage=resistant)
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FOORI; CDNA made by Oligo-dr priming. Directionally
Cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G): Size_reslected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
37 a 241c 283 g 203 t
                                                                                                                                                                                                                                                      BG281831 964 bp mRNA linear EST 21-FEB-2001 602403057F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4545302 5',
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 96)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCID/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: image.llnl.gov Plate: LLCM1230 row: a column: 15
High quality sequence stop: 659.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 agcgtgggaaggagcggaccetgctctccccgggctgcgggccatggccac-ggcggagc 119
                                      22 AGGACCCGCGAGGAAGGGCCCGCGGATGGCGCGTCCCTGAGGGTCGTGGCGAGTTCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 aggacccgcgaggaagggcccgcggatggcgcgtccctgagggtcgtggcgagttcgcgg
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Pred. No. 3.6e-71;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                     BG281831.1 GI:13030757
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Best Local Similarity 98.3%;
Matches 641; Conservative
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BG281831
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='InAGE:394814"
/clone='InAGE:394814"
/clone='InAGE:394814"
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//ab_host="BH108 (phage-resistant)"
/note="organ: oversy: Vector: poTB7; Site_1: XhoI: Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                              Couract, nower, stransbergy, Filt.D.

Finall: cgapbs refemal inih, gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM810 row: n column: 19

High quality sequence stop: 711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gttggtgtgaaagatttcaatgagacacagctggcccggattgcggacagtaaggatcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtgtttcccgtgaatgacggctttcaggctctgcaaggcatcatccactcaattttgaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Pred. No. 8.5e-79;
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                      Contact: Robert Strausberg, Ph.D.
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  Unpublished
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Matches 653;
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/clone_lib="HT0209"
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/note="Corgan: head_neck; Vector: pucl8; Site_1: Smal;
Site_2: Smal, A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRO-HT0209-280300-106-b03 HT0209 Homo sapiens cDNA, mRNA sequence.
BE146075
BE146075.1 GI:8608799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W.Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gatggcgcgtccctgagggtcgtggcgagttcgcggagcgtgggaaggagcggaccctgc
                                                                                                                                                                                                                                                                                                              teteccegggetgegggecatggccacggcggagcggagagccctcggcatcggetteca
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                                                                                                                                                                                                                             Length 513;
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Pred. No. 7.8e-59;
0; Mismatches 5;
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150 c 127 g 128 t
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Best Local S
Matches 496
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1 (bases 1 to 513)

1 (bases 1 to 513)

Dias Ne., Garcia Orrea, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da 511va, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/cripts/gethtml2.pl?tl-&t2-MRO-HT0209-280 300-106-909&t3-2000-03-28&t4-1) Seq primer: puc 18 forward High quality sequence start: 21 High quality sequence start: 21 High quality sequence storp: 513.
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MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                acttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattac-ttt
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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MRO-HT0209-280300-106-909 HT0209 Homo sapiens CDNA, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE146084.1 GI:8608808
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                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0209-280
300-106-b03&t3=2000-03-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 51
High quality sequence start: 51
Location/Qualifiers
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                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Shotgun sequencing of the human transcriptome with ORF expressed
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            sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 5.5e-56;
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99.2%;
                                                                                                                      rel: +55-11-2704922
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/organism="Homo sapiens"
/db_zerf="texan:9606"
/do-stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
bE146355
MRO HT0209-010500-110-f09 HT0209 Homo sapiens CDNA, mRNA sequence.
BE146355
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                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 3.8e-54;
0; Mismatches 5;
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Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
                                                                                                           BE146355.1 GI:8609079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
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BM050390 569 bp mRNA linear EST 07-NOV-2001 603632635F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5423217 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 569)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1882 row: e column: 10
High quality sequence stop: 569.
Location/Qualifiers
1. .569
                         675 ttgcggacagtaaggatcatgtgtttcccgtgaatgacggctttcaggctctgcaaggca
1 TCAGGAAGTGTGCTGCACCACTGGAATGAAATCTACTACTTCGTGGAGCAGCTGGCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                855 acgtggacagggtcctctgcagcttcaagatca 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BM050390
BM050390.1 GI:16779657
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Muses 1 to 638)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/organism="Mus musculus"
/organism="Mus musculus"
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/lab_host="DH10B"
              tgggggtccagcctgctacggcggatttgacctgtacttcattttggacaaatcaggaag
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85.8%; Pred. No. 1.3e-52;
ive 0; Mismatches 86;
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BE369415.1 GI:9314778
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      /clone_lib="NHLMGE:43217"
/clone_lib="NHLMGE:43217"
/clone_lib="NHLMGC_43"
/clone_lib="NTHLMGC_43"
/clone_lib="NTHLMGC_43"
/lab_host="DH10B [phage-resistant)" is the liberation of the liberation of the liberation of the liberation of the liberation of the liberation of deraid M. Rubin (University of California, Berkeley) using Zah-coha synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

39 a 140 c 181 g 109 t
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mRNA sequence.
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Catarrhini; Hominidae;
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MRO-HT0209-100100-103-f09 HT0209 Homo sapiens CDNA,
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                 Length
                                                                                                                                                                                                            Score 432; DB 10;
Pred. No. 1.8e-50;
0; Mismatches 10;
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 465)
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BE145958.1 GI:8608682
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al Similarity 95.7%;
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Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0209-100 100-103-f09&t3=2000-01-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="HTT0209"
//dev_stage="Adult"
/note="Organ: head_neck; Vector: puci8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - budwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                          expressed
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                                                                                           (7), 3491-3496 (2000)
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Pred. No. 8.3e-49;
0; Mismatches 13
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                                                                                         U.S.A.
                                                                                         Sci.
                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.7%;
Best Local Similarity 96.9%;
Matches 439; Conservative 0
                                                                                         Proc. Natl. Acad.
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Mashington University School of Medicine
Mat44 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539 bp mRNA linear EST 15-MAR-2000 mg81d04.yl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA al466645
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R., Cardenas, M., McCann, R., Materston, M. and Wilson, R., Mordan, M., McCann, R., Materston, M., Mouse EST Project 1999
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                                                                                                                                                 396 acagagaacaaatccgtcaaggcctagaagaactccagaa-agttctgccagga-ggaga
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                                                               319 ACTGGAATGAAATCTATTACTTGGTGGAACAGTTGGCTCACAAAATTCATCAGCCCACAGT
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:439399"
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/clone_inp="NIH_MGC_i14"
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ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCGAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
Callfornia, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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1 (bases 1 to 693)

NTH-MGC http://mgc.nci.nih.gov/.

NTH-MGC http://mgc.nci.nih.gov/.

Gontact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: DCTD/DTP

Tissue Procurement: DCTD/DTP
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM4268 row: n column: 23
High quality sequence stop: 571.
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Matches 419; Conservative
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Human metastasis a Human immune syste Human immune syste Tumour suppressor Human immune syste

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Human; secreted protein; proliferative disorder; cancer; tumour; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; skin disorder; psoriasis; sepsis; disbetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cendocrine disorder; pregnancy-related disorder; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19; ss.
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           AAL25878
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                      Compugen Ltd.
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                                                                                                                                                                                                            1736436 seqs, 858457221 residues
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Copyright (c) 1993 - 2000 Comp
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Human immune syste Human immune syste Macaque TANGO 232

Tumour suppressor

"Human secreted protein"

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Tumour suppressor

Chemically pretrea Human immune syste Human immune syste

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And Androis 300-Androis 379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing the the rew protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the control for the new genes. Specific uses are described for each of the most of the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disorders, cardioase), cognitive disorders, schizophrenia, asthma, cardioascapes, or disease), sepsis, diabetes, atheroscierosis, cardioascapes, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound callsoried to primary tissues, to regenerate tissues, to identify their colluture of primary tissues, to regenerate tissues, to identify their contract light of the properties.
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Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid molecules encoding 28 human secreted proteins for {\it shoot} proventing, treating or ameliorating medical conditions and
/product= "Mature human secreted protein'
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2000US-0215133.
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30-JUN-2000;
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Gaps 09 aggacccgcgaggaagggccgcgggatggcgtccctgagggtcgtggcggttcgcgg 2447; . 0 Length 4; Indels 22; DB Score 1193.6; DB Pred. No. 3e-283; Mismatches ; 84.4%; 99.7%; Conservative Similarity Query Match Best Local Simi Matches 1196; Н

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1020 720 756 780 900 360 420 456 480 540 900 989 969 300 336 tgaaccatccaccatatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt ccgacatgcccgcaacgtggacaggtcctctgcagcttcaagatcaatgactcggtcac ctgcactgtgattatcaaggaggtccctccacccctgccgaggagagtgaggaaaataa ggaacagttggctcacaaattcatcagcccacagttgagaatgtcctttattgttttctc acagctggcccggattgcggacagtaaggatcatgtgtttcccgtgaatgacggcttca cgggcaaggggacgcagggaggatgggggtccagcctgctacggcggatttgacctgta 217 cgggcaagggggacgcagggaggatgggggtccagcctgctacggcggatttgacctgta cttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctatttgt 817 266 1057 1117 1141 697 841 901 1021 1081 541 601 637 661 781 961 241 361 397 421 457 301 QQ g g 셤 Dp δŽ g οy 셤 ŏ a δŏ g qq QΥ g δ g δ g δ δ Q δ δ ò ŏ a g δy δy

AAD05334 standard; cDNA; 2086 AAD05334

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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE0146-AAE01513 represent the proteins they encode. AAE01544-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. It herapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the case passed on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities; haematopoietic disorders, diseases of the immune system, allergies, neurological disorders (e.g., Alzheimer's disease, albeaner's disease, parkinson's disease), cognitive disorders, schizophrenia, asthma,
                                                                                                       Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumaton; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19; ss.
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/transl_except= (pos:1156..1158, aa:Xaa)
/transl_except= (pos:1267..1269, aa:Xaa)
/note= "Xaa equals any of the twenty naturally ocurring
L-amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                       Human secreted protein-encoding gene 4 cDNA clone HWLFR02, SEQ ID NO:45
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/product= "Mature human secreted protein"
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AAD05334;
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skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell colluture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food addittive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioinmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.
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el nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, and 239 polypeptides useful for the treatment of asthma, rheumatoid
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prognosis; prophylatic; therapeutic; human; ds
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postnasis, inflammatory bowel disease, septic shock, ulcerative colitis, Corbn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cacheria and autoimmune disease, osteoarthritis, Lyme's disease, cacheria and autoimmune disease, e.g. myasthemia gravis, autoimmune diabetes and systemic upus erythematosus. The nucleic acids are also useful for producing Langeonic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, paramacogenomics and for monitoring clinical trials. TANGO pharmacogenomics and for monitoring clinical trials. TANGO comprehenses are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
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Pred. No. 1.5e-248;
0; Mismatches 1;
arthritis, psoriasis and autoimmune diseases
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                       Claim 1; Fig 4; 209pp; English
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Best Local Similarity 99.9%;
Matches 1053; Conservative
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                                                                                                                                                                                                                                                                                             Human, nootropic, immunosuppressant, cytostatic; gene therapy, cancer peripheral nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
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                     CCGacatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcac
                                                                                                                         tgaaccatccaccatatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt
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Zhang J
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Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous to localised neuropathies and central nervous system diseases, such as catarial sclerosis, and Shy-Drager Syndrome. Other uses include the cullisation of the activities as uch as: Immune system suppression, and thrombolytic activity, chemotacilc/chemoKinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and conter the sequence data for this and inflammation, leukaemias and localistic the sequence data for this context.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; cancer;
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                                                          tgaaccatccaccatatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt
 acagetggeceggattgeggacagtaaggateatgtgttteeegtgaatgaeggetttea
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Drmanac RT;
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Zhou P, Goodrich R,
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Zhao QA,
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Wang J,
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Ackleiner's, Parkinson's disease, Huntington's diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemoteactic/chemokinetic activity, neamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                    The sequence data for this patent did not form part of the printed
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99.8%; Pred. No. 7.6e
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full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide sequences defined in the specification, where the

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 3'-end sequence, where the

coligonucleotide which comprises at 1-end is selectides on the combination of

the 5'-end sequence 3'-end sequence 15 selectides and the combination of

the 5'-end sequence 3'-end sequence 15 selectides and the combination of

the specification. The primers at useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers and NAH13618 and

ANH13631 to AAH18412 represent human cDNA sequences; AAH3416 to

ANH3631 to AAH18412 represent human cDNA sequences; and AAH13622
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                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy;
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Otsuki
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A, Nagai
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T, Wakamatsu
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11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-02418997.
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Length 1436;
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890; DB 22;
No. 9.7e-209;
                   Mismatches
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99.3%;
                    Conservative
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postriasis, inflammatory bowel diseases, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoathritis, Lyme's disease, cachexia and autoimmune disease, e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial Crangoli28, 140, 197, 213, 213, 214, 239 sequences are useful in for ensic biology, for diagnostic assays, prognostic assays, paramacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a clisorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                      TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host disease; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; lyme's disease; cachexita; altroimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   producing
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3.1148
/*tag= a
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/product= TANGO 197
                                                                                                                             Murine TANGO 197 coding sequence.
                 standard; cDNA; 4417 BP
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P-PSDB; AAB01428.
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
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                                  Yamamoto
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                     Human cDNA clone (5'-primer) SEQ ID NO:3023.
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A, Nagai K
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Sugiyama T, Wakamatsu
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                                                                                                                                                                                                                                                                                                    standard; cDNA; 464
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27-AuG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
09-JUN-2000; 2000JP-02418999.
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                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Gaps

Score 453.2; DB 21; Length 4417; Pred. No. 3.6e-101; 0; Mismatches 53; Indels 0;

Query Match 32.1%; Best Local Similarity 90.1%; Matches 485; Conservative (

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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oilgo-dT primer and an oilgouncleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oilgonucleotide comprises a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oilgonucleotide comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide comprises a 1-east 15 nucleotides and the complementary
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH1872 tepresent human cDNA sequences?

AAH13633 to AAH1872 tepresent human cDNA sequences?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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Sequence 464 BP; 101 A; 122 C; 141 G; 90 T; 10 other;

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                                                           53 ggaaaggcccgcgggatggcgcgtccctgagggtcgtggcgagttcgcggagcgtgggaag 112
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                                                                                                                                                                                                                                                                                                 Length 464;
                      24; Indels
Score 368; DB 22;
Pred. No. 1.1e-80;
0; Mismatches 24;
26.0%;
93.9%;
                    Matches 388; Conservative
 Query Match
Best Local Similarity
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Length 356;

DB 22; 4.7e-76;

Score 349; DB Pred. No. 4.76

24.7%; Scor 100.0%; Pred 0; N

Conservative

Query Match Best Local Similarity Matches 349; Conserv

Sequence 356 BP; 91 A; 78 C; 95 G; 92 T; 0 other;

635 127 695 187 755 247 815 307

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516 ggtacaggacagccagcgtcatcattgctttgactgatggagaactccatgaagatctct 8 ggtacaggacagccagcgtcatcattgctttgactgatggagaactccatgaagatctct

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tgtttcccgtgaatgacggctttcaggctctgcaaggcatcatccactcaattttgaaga
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                                                                                                           AAL08133 standard; cDNA; 355
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Human breast cancer expressed polynucleotide 11500. Human; breast cancer; cell marker; cytostatic; ss.

Homo sapiens

(first entry)

07-DEC-2001 AAL19043;

SX KX DX AX

AAL19043 standard; cDNA; 356

AAL19043 RESULT

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The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                            New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                               Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 2056; 3695pp; English.
                                                                                                                                    24-MAR-2000; 2000US-0192099.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-0205230.
09-JUN-2000; 2000US-0211315.
                                                                                                                                                                                                   25-JUL-2000; 2000US-0220534
                                                                         2001WO-US00798
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             WO200151628-A2
                                                                         10-JAN-2001;
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                                          19-JUL-2001
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standard;
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25-JUL-2000;
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                             AAL25878
                                                   AAL25878;
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Matches 34
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                    AAL25878
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                                                                                                                                                                                                                                                                                                                                                                    invention relates to human breast cancer expressed polynucleotides
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                                                                                                                                                                                                                                                                                                                     peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 355 BP; 91 A; 78 C; 94 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.6%; Score 348; DB 22;
100.0%; Pred. No. 8.3e-76;
ive 0; Mismatches 0;
                     Human breast cancer expressed polynucleotide 590.
                                           breast cancer; cell marker; cytostatic;
                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                           Steinmann K;
                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                    2000US-0189167.
2000US-0192099.
2000US-0193480.
2000US-0205230.
2000US-0211315.
                                                                                                                                    10-JAN-2001; 2001WO-US00798
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                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 189; 3695pp;
07-DEC-2001 (first entry)
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nes 348; Conserv
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                                                                                        WO200151628-A2.
                                                                                                                                                                                           29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
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                                                                   Homo sapiens
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24-MAR-2000;
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(AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynocleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynocleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                         polynucleotide 18335.
                                                                                                                                                                    Human; breast cancer; cell marker; cytostatic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide useful as a marker for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.5%; Score 346; DB 22;
100.0%; Pred. No. 2.6e-75;
ive 0; Mismatches 0;
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BP.
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CDNA; 346
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24-MAR-2000; 2000US-0192099.
29-MAR-2000; 2000US-0193480.
19-MAY-2000; 2000US-0205230.
09-JUN-2000; 2000US-0211315.
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                                                                                                                                                                                                                                                                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; aclectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiactasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; tatrogenic disease; inflammation; meningitis;
Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human TANGO 216 polypeptide. The present sequence encodes a human TANGO 261, TANGO 262, and TANGO 267. The TANGO 262, and TANGO 267. The TANGO Polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand catotr-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema,
Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
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                                                                  819 ttgtcgtgagagaaacggcttccgacatgcccgcaacgtggacag
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chronic bronchitis, bronchial asthma and bronchlectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, istrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
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Disclosure; Page -; 175pp; English.
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                          844 acatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcacact
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AAA75157-59 encode human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO consists of the cellular proliferation, modulate polypeptides can be used to modulate cellular adhesion. The cellular adhesion and/or modulate cellular adhesion. The discorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematropoietic associated diseases and disorders, atelectasis, confestion or oedema, emphysema, chronic bronchitis, bronchitis, bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as isohemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated with the owaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, alzheimer's Disease, inflammations, thydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
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nes 671; Conservative
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Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, an for trasting cancer.

262, 266 and 267 useful a e.g. for treating cancer

Fraser CC;

Sharp JD,

Sarnes TM, Holtzman DA,

WPI; 2000-579269/54. P-PSDB; AAB18456.

(MILL-) MILLENNIUM PHARM INC.

01-MAR-2000; 2000WO-US05226.

08-SEP-2000

99US-0122458.

01-MAR-1999;

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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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cartibes TANGO 266, TANGO 262, and TANGO 267. The TANGO 267 cartibes TANGO 266, TANGO 267, and TANGO 267. The TANGO 267 callular differential unique in and/or modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cellular interactions, and cell trafficking and/or migration, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, confidential and hematopoietic associated diseases and disorders, spleen associated diseases and disorders, spleen associated diseases, modulate the proliferation, differentiation, as ischamic heart disorders, intestinal disorders, spleen associated cliesases, modulate the proliferation, differentiation, as ischamic heart disease, modulate the proliferation, differentiation, as ischamic heart diseases, modulate the proliferation of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder, and cerebral ocdema, hydrocephalus, brain herniations, latrogenic disease, inflammations, concernial and viral meningits, Alzheimer's Disease, cerebral cancers, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Concert the present sequence does not appear in the specification; it was concert and meninging concerns and care descended ones not appear in the present sequence does not appear in the specification; it was
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ive 0; Mismatches
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TISSUE SPECIFICITY: Highly expressed in tumor endothelial cells but not in normal endothelial cells.

DOMAIN: Blading to PA seems to be effected through the VWA domain. SIMILARITY: BELONGS TO THE ATR FAMILY.

SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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CA17_HUMAN
CFAB_MOUSE
CA26_MOUSE
CAMA_MOUSE
MTN2_MOUSE
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ATR_MOUSE
CMG2_HUMAN
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CA1C_MOUSE
CO2_MOUSE
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MTN4_MOUSE
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CA36_HUMAN
DNAK_NEIMB
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Maximum Match 100%
Listing first 45 summaries
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ITAM_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                      TRGTTLMKLTEDREQIRQCLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
EDDD -> NKIK (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
NEKPFSVEDTYLLCPAPILKEVGMKAALQV -> SKSLQS
                                                                                                                                                                                                                                           MISSING (IN ISOFORM 3).
DGSILAIALLILFLL -> LHKIASGPTTAACME (IN
                                                                                                      Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                  LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS 295
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                                                                                                                                                                                                                                                                                                      100.0%; Score 1536; DB 1; Length 564; 100.0%; Pred. No. 6.1e-120;
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01-MAR-2002 (Rel. 41, Last annotation update)
Antrax toxin receptor precursor (Tumor endothelial marker 8).
ATR OR TEM8.
                                                                                                                                                              ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                      ANTRAX TOXIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                            ISOFORM 4).
MISSING (IN ISOFORM 4).
B118A00AD5DF2233 CRC64;
                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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                                                                                                                                         POTENTIAL
                                    EMBL, AF279145; AAK52094.1; -.
EMBL, AK029429; BAB15128.1; ALT_INIT.
EMBL, AK001463; BAB1707.1; ALT_FRAME.
EMBL, BC012074; AAH12074.1; -.
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                                                                            Interpro: IPR002035; vWFA.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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Best Local Simi
Matches 295;
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                                                                                                                                                                                                                                                                                                                          RA Kawai J., Shibadaa K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Brinadaa R., Yoshino H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Erkunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Satio T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonada M. F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Saski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Winshaw-Borts A., Yoshida K., Haseqawa Y., Rawaji H., Rohtsuki S.,
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
GRCINFTRVKNSQPAKYPLNNTYHSSSPPRAPIYTPPPPAP
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SUBCELULAR LOCATION: Type I membrane protein (Probable).
ALTERNATIVE PRODUCTS: 2 isocorms; 1 (shown here) and 2; seem to be produced by alternative splicing.
DOMAIN: Binding to PA seems to be effected through the VWA domain
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SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
SIMILARITY: BELONGS TO THE ATR FAMILY.
SIMILARITY: CONTAINS I VWFA DOMAIN.
                                                                                                                                                                                                                                                         SEQUENCE OF 88-562 FROM N.A. (ISOFORM 2).
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EMBL; AK013005; BAB28591.1; ALT_INIT.
                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-Embryo; MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                            Cancer Res. 61:6649-6655(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62308 MW;
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                                                                                                                      basement
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                                                                            25 GHGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHRFISPQLRMSFIVFS
                                                              1 GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                                                                                 181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A MEDILINE-2153956;.
A MEDILINE-2153956;.
A Maxwell S.R., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
A Maxwell S.A., Davis G.E.;

"Differential gene expression during capillary morphogenesis in 3 collagen matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.";

J. Cell Sci. 114:2755-2773(2001).
C -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
C -!- SIMILARITY: BELONGS TO THE ATR FAMILY.
C -!- SIMILARITY: CONTAINS I VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                            241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS 295
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0F9B2D6688EAB17A CRC64;
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 Length 562;
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                                 Indels
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capillary morphogenesis protein-2 precursor (CMG-2).
Score 1519; DB 1;
Pred. No. 1.6e-118;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    386 AA
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   98.98;
                                 Conservative
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Eukaryota; Metazoa;
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211
386 AA;
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               Local Similarity
es 291; Conser
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P58335;
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SEQUENCE
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MEDLINE=99059842; PubMed=9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
Hoffman P.A., Staunton D.E., Bochner B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1
                                                                                                                                                                                                                                                                                                                                                                                                                    144 IALTDGKLDGLVPSYAEKEAKISRSLGASVYCVGVLDFEQAQLERIADSKEQVFPVKGGF 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Splead.
MEDLINE-96111956; PubMed-8777714;
Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M.;
**A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-3."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the leukocyte integrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99370002; PubMed-10438935;
Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITAD_HUMAN STANDARD; PRT; 1162 AA. 015379; 015575; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015
                                                                                                                                                                26 GPGGLLRAQEQPSCRRAFDLYFVLDKSGSVANNWIEIYNFVQQLAERFVSPEMRLSFIVF
                                                                                                                                                                                                                                                                                             120 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGF
                                                                                                                                1 GQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVF
                                                                                                                                                                                                                                                         60 STRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
"Cloning and chromosomal localization of a novel gene-encoding beta 2-integrin alpha subunit.";
Gene 171:291-294(1996).
   Length 386;
                                                                    Indels
      DB 1;
                                                              43;
                                    .4e-37
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MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of speece CD11d. Essential role of Sp1 and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
34.8%; Score 534.5;
llarity 57.1%; Pred. No. 4.4e
Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exp. Med. 188:2187-2191(1998).
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                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 QALQGIIHS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 QALKGIINS 212
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                                       Local Simi
         Query Match
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                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein.

-1. SUBCELLULAR LOCATION: Type I membrane protein.
-1. SUBCELLULAR LOCATION: Type I membrane protein.
-1. SUBCELLULAR LOCATION: Type I membrane protein.
-1. TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL
LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGIY ON TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.
-1. DOMAIN: THE INTEGRIN I LOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-1. SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-1. SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
"The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding interface between I domain and VCAM-1.";
J. Immunol. 163:1984-1990(1999).
-!- FUNCTION: INTEGRIN ALPHA-D/PETA-2 IS A RECEPTOR FOR ICAM3 AND VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS CLEARING LIPOPROTEINS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOODBORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES FROM THE BLOOD.
                                                                                                   SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; WWFA; 1.
Integrin; Cell adhein; Receptor; Glycoprotein; Transmembrane;
Signal; Repeat; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FG-GAP 1.
FG-GAP 2.
WWFA.
FG-GAP 4.
FG-GAP 4.
FG-GAP 5.
FG-GAP 5.
FG-GAP 7.
PG-GAP 7.
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EMBL, U40274; AAB60534.1; --
EMBL, U40275; AAB60635.1; --
EMBL, U40276; AAB60635.1; --
EMBL, U40277; AAB60637.1; --
EMBL, U40278; AAB60638.1; --
EMBL, A40278; AAB60638.1; --
EMBL, AF187881; AAF62875.1; --
HSSP; P11215; 1A8X.
MIN; 602453; --
InterPro; IPR00413; Integrin_alpha.
InterPro; IPR00413; INtegrin_alpha.
InterPro; IPR002035; vWFA.
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Pfam; PF00092; vwa; 1.
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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MEDLINE-88190151; PubMed-2833753;
Arnaout M.A., Remold-O'Donnell B., Pierce M.W., Harris P., Tenen D.G.;
"Molecular cloning of the alpha subunit of human and guinea pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE-88315033; PubMed-2457584; Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.; Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.; The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B."; J. Biol. Chem. 263:12403-12411(1988).
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01-CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1ntegrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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SEQUENCE FROM N.A.
MEDLINE-88257215; PubMed-2454931;
Arnaout M.A., Gupta S. K., Pierce M.W., Tenen D.G.;
Anno acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
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MEDLINE-95171458; PubMed-7867070;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integrin
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MEDLINE-96363671; PubMed-8747460;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                           MEDLINE-93123748; PubMed-8419480; Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.; "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation genomic organization and suggest early diversification during
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Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
leukocyte adhesion glycoprotein Mol: chromosomal localization and
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Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
N. terminal sequence of human leukocyte glycoprotein Mol:
conservation across species and homology to platelet IIb/IIIa.";
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; PubMed=1683702;
Shelley C.S., Arnaout M.A.;
He promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92144986; PubMed-1346576;
Pahll H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
            homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
                                                                                                                                                                                                                                              SEQUENCE OF 9-1153 FROM N.A. MEDLINE-89098893; PubMed-2563162;
                                                                                                                                                                                                                     Immunol. 150:480-490(1993).
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Cell 80:631-638(1995).
                                                                                                                                    SEQUENCE FROM N.A.
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MEDLINE-98256734; PubMed-9560195;

MEDLINE-98256734; PubMed-9560195;

Oxvig C., Springer T.A.;

RT "Experimental support for a beta-propeller domain in integrin alpha-
RT subunits and a calcium binding site on its lower surface.";

PROC. Natl. Acad. Sci. US.A. 95:4870-4875 (1998)

RE PROC. NATL Acad. Sci. US.A. 95:4870-4875 (1998)

C. I- FUNCTION: INTEGRIN ALPHA-N/BETA-2 IS IMPLICATED IN VARIOUS

AS WELL AS IN MEDIATING THE UPTAKE OF COMPLEMENT-COAFED PARTICLES.

IT IS IDENTICAL WITH GR-3. THE RECEPTOR FOR THE IC13B FRAGMENT OF

THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECOGNIZES THE R-G-D

PEPTIDE IN CASE INTEGRIN ALPHA-N/BETA-2 IS ALSO A RECEPTOR FOR

FIBRINOGEN, FACTOR X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES

OF FIBRINOGEN, FACTOR X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES

OF FIBRINOGEN, FACTOR X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES

OF SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-M

ASSOCIATES WITH BETA-2.

ILSUBLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                               -!- DOMAIN. THE INTECRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTECRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS I VWFA BOMAIN.
-!- SIMILARITY: CONTAINS 7 FG-AP REPEATS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd11b.htm".
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EMBL; M84477; AAA51960.1; -
PIR; A31108; RWHUIB.
PIR; A26091; A26091.
PDB; 1A8X; 17-JUN-98.
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AAA59903.1;
AAB24821.1;
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S52213;
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S52219;
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S52203;
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PIR; A36584; RWHUIC.
HSSP; P11215; 1A8X.
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MEDLINE-8816645; Pubmed-3327687;
Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
"cDNA cloning and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95.";
EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu M5).
ITGAX OR CD11C.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      Interfroit integrin_A; 1.

Pfam; PF01839; FG-62P; 5.

Pfam; PF00357; integrin_A; 1.

Pfam; PF00092; vwa; 1.

PRINTS; PR01185; INTEGRINA.

PRINTS; PR01185; INTEGRINA.

SMART; SM00191; Int_alpha; 4.

SMART; SM00191; Int_alpha; 4.

PROSITE; PS00242; INTEGRIN_ALPHA; 1.

PROSITE; PS50234; VWFA; 1.

Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1152;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 145.5; DB 1;
; Pred. No. 0.00032;
45; Mismatches 81;
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InterPro; IPR002035; vWFA.
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les 60; Conservative
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                                                                                              CarbBank; CCSD:33581; -. CarbBank; CCSD:33582; -. CarbBank; CCSD:33584; -.
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1152
1104
1128
1152
                     18-NOV-98.
25-NOV-98.
01-AUG-96.
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P20702;
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1IDO;
     1BHO;
                                                                              PDB; 1JLM;
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TRANSMEM
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ITAX_HUMAN
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECOGNIZES THE SEQUENCE G-P-R IN FIRRINGEN. IT MEDIATES CELL-CELL INTERACTION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY IMPOROTRANT IN MONOCYTE ADHESION AND CHEMOTAXIS.
SUBBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-X ASSOCIATES WITH BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-:- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-:- SIMILARITY: CONTAINS I VWFA DOMAIN.
-:- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
-:- DATABASE: NAME=PROW; NOTE-CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΙŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and p150,95 leukocyte adhesion proteins.";
J. Immunol. 138:2381-2383(1987).
-!- FUNCTION: INTEGRIN ALPHA-X/BETA-2 IS A RECEPTOR FOR FIBRINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 20-43.
MEDLINE-87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
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PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
MEDLINE-90153906; PubWed-2303426;
Corbl A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                  rbi A.L., Garcia-Aguilar J., Springer T.A.;
Biol. Chem. 265:12750-12751(1990).
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EMBL; Y00093; CAA68283.1; -.
EMBL; M29165; -; NOT_ANNOTATED_CDS.
EMBL; M29487; AAA51620.1; ALT_SEQ.
EMBL; M29483; AAA51620.1; JOINED.
EMBL; M294843; AAA51620.1; JOINED.
EMBL; M294845; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
EMBL; M294865; AAA51620.1; JOINED.
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InterPro; IPR002035; vWFA.
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                                                                                                                                                    Biol. Chem. 265:2782-2788(1990)
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Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
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PRINTS; PR00453; WPFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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PTM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND----IASKPSQEHIFKVED- 318
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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-> D (IN REF. 2).
6C4E19CC3F62A473 CRC64;
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01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain precursor (Fibrochimerin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 143.5; DB 1
24.8%; Pred. No. 0.00048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Mismatches
                                                    FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
POTENTIAL.
POTENTIAL.
GFFKR MOTIF.
 CYTOPLASMIC
            FG-GAP 1.
FG-GAP 2.
VWFA.
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STRAIN-WHITE LEGHORN;
MEDLINE-92011862; PubMed-1918137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C_CHICK
CAIC_CHICK
D13944; 004509;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1997 (Rel. 35, Last seque
                                                                                                                                                                                                                                                                                                                                                                                                                                      127885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Conservative
                                                                                                                                                                                                                                            863
1022
1032
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490 49
756 75
1163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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NCBI_TaxID=9031;
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CA_BIND
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                                        DOMAIN
                                                                     REPEAT
REPEAT
REPEAT
DOMAIN
                            REPEAT
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MEDINE-95370352; PubMed-7642694;
MEDLINE-95370352; PubMed-7642694;
MCOCH M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
MCOCH M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
MCOCH M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
MCCH BIOL 1301005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-101005-1
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"The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifis, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type ix collagen, and short collagenous domains with an Arg-Gly-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS, .
LIGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE
TISSUES CONTAINING TYPE I COLLAGEN.
DOMAIN: THIS SEQUENCE DEFINES FIVE DISTINCT DOMAINS, TWO TRIPLE-
DELICAL DOMAINS (COLL AND COL2) AND THREE NONTRIPLE-HELICAL
DOMAINS (NC1, NC2, AND NC3).
PTW: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
EACH END.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2846-2873.
MEDLINE-90062079; PubMed-2584192;
Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.;
"Type XII collagen. A large multidomain molecule with partial homology to type IX collagen."
J. Biol. Chem. 264:19772-19778(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2960-3076 FROM N.A.
MEDLINE-87317590; PubMed-3476925;
Gordon M.K., Gerecke D.R., Olsen B.R.;
"Type XII collagen: distinct extracellular matrix component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovered by cDNA cloning.";
Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=93042014; PubMed=1420368;
                                                                                                                                                                                                                                                                                                      Cell Biol. 115:209-221(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trueb J., Trueb B.;
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14;

Gaps

36;

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01-NOV-1988 (Rel. 09, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
                                                                                                                                                                                                                                                                                                     131 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHS 188
                                                                                                                                                                                                               75 QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 130
                                                                                                                                                                                         18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C; TISSUE-Spleen, MEDIINE-86287312; PubMed-2942940; MEDIINE-86287312; PubMed-2942940; Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E., Larson R.S., Roberts T.M., Springer T.A.; T.A. partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1."; proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                      189 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-86188276; PubMed-3887182; Springer T.A., Teplow D.B., Dreyer W.J.; Squence homology of the LFA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon."; Nature 314:540-542(1985).
                                                                                                                                ; Score 143; DB 1; Length 3124;
; Pred. No. 0.0019;
51; Mismatches 97; Indels 31
          T -> S (IN REF. 4).
D -> E (IN REF. 4).
P -> A (IN REF. 2).
L -> F (IN REF. 2).
V -> F (IN REF. 3).
QP -> AG (IN REF. 3).
QP -> AG (IN REF. 3).
ISOFORM).
SHORT
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MISSING (IN
                                                                                                                                        9.3%; Score 143; 26.1%; Pred. No. 0
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MEDLINE=88312584; Pubmed=3044779;
                                                                                               340578
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                                                                                                                                                                   65; Conservative
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1188
1258
1264
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2803
2803
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                                                                                                AA;
                                                                                                                                                      Best Local Similarity
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ID ITAM_MOUSE

AC P0555;

DT 01-NOV-1988 (DT 01-FEB-1991 (
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PRINTS; PR004014; ENTYPEIII.
PRINTS; PR00453; VWADOMAIN.
SMART; SM00060; FN3; 17.
SMART; SM003010; TSPN; 1.
SMART; SM00327; vWar, 4.
PROSITE; PS50234; VWRP, 4.
PROTECTION Collagen; Signal; Glycoprotein; Alternative splicing.
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTIFICAL REGION (NC2).
TRIPLE-HELICAL REGION (NC2).
WITH 2 INVERFECTIONS.
NONHELICAL REGION (NC1).
ASP/GLU RICH (ACIDIC).
ARC/LYS-RICH (BASIC).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENY SITE (POTENTIAL).
CELL ATTACHMENY SITE (POTENTIAL).
CELL ATTACHMENY SITE (POTENTIAL).
CELL ATTACHMENY SITE (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
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N-LINKED GLCNAC...)
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FIBRONECTIN TYPE-III 14
FIBRONECTIN TYPE-III 15
FIBRONECTIN TYPE-III 15
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FIBRONECTIN TYPE-III
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FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                        VWFA 2.
FIBRONECTIN T
                                                                                                            InterPro; IPR00087; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003129; TSPN.
InterPro; IPR002035; vWFA.
Ffam; PF00041; fn3; 17.
Ffam; PF02210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                             VWFA
  ; D00824; BAA00701.1; -.
x61024; CAA43358.1; -.
M17375; AAA48718.1; -.
J05137; AAA48655.1; -.
x67327; CAA47744.1; -.
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3048
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1006
1032
1044
1512
1767
2210
2273
2532
                                                          EMBL; X67327; CAA47744
PIR; A28037; A28037.
PIR; A34485; A34485.
HSSP; P17301; 1AOX.
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Query Match
Best Local Similarity 24.28
Best Local Similarity 71: Conservative
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86
391
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-i- FUNCTION: INTEGRIN ALPHA-M/BETA-2 IS IMPLICATED IN VARIOUS
ADHESTYE INTERACTIONS OF MONOCYTES, MACROPHAGES AND GRANULOCYTES
AS WELL AS IN MEDIATING THE UPTAKE OF COMPLEMENT-COAPED PARTICLES.
IT IS IDENTICAL WITH CR-3, THE RECEPTOR FOR THE IC3B FRAGMENT OF
THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECOGNIZES THE R-G-D
PETTIDE IN C3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR
FIBRINOGEN, FACTOR X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES
OF FIBRINOGEN GAMMA CHAIN. ALPHA-M/BETA-2 PLAY A CRITICAL ROLE IN
MAST CELL DEVELOPMENT AND IN IMMUNE COMPLEX-MEDIATED
GLOMERULONEPHRITIS. MICE EXPRESSING A NULL MUTATION OF THE ALPHA-M
SUBUNIT GENE DEMONSTRATE INCREASE IN NEUTROPHIL ACCUMULATION, IN
RESPONSE TO A IMPAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT
                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                           -i- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-i- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-i- SIMILARITY: CONTAINS I VWFA DOMAIN.
-i- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                                                                                                                                                             ASSOCIATES WITH BETA-2.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                   SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M
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FG-GAP 4.
FG-GAP 5.
FG-GAP 7.
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FG-GAP 2.
VWFA.
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InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
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PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 4.
SWART; SM00327; VWA; 1.
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Pfam; PF00357; integrin_A; 1.
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1105
1129
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84
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HSSP; P11215; 1A8X.
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150 DIVFLIDGSGSI----NNIDF---QKMKEFVSTVMEQFKKSKTLFS-----LMQYSDEFR 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT 257
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SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%: Score 141; DB 1; Length 1153; 24.2%: Pred. No. 0.00077; ive 50; Mismatches 96; Indels 7
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15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain precursor.
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                                                                                                                                                                                                                                                                                                     PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: CONTAINS 4 VWFA DOMAINS.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TRENDONS, PERICHONDRIUM, SICHERA, BLOOD VESSELS, AND PERIOSTEUM.

DEVELOPMENTAL STAGE: LONG FORM OF COLLAGEN XII, XIIA, IS THE PREDOMINANT FORM AF EARLY STAGES (ED? AND 11); AT LATER STAGES OF DEVELOPMENT (ED15 AND 17) THE SHORT FORM BECOMES THE MAJOR PRODUCT, THE LONG SPLICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIRINE; FROOD14; VENTYPEIII.
PRINTS; PROOD15; VWFADOMAIN.
SMART; SMOOD60; FN3; 16.
SMART; SMO0210; TSPN; 1.
SMART; SMO0327; VWA; 4.
PROSITE; PS50234; VWPA; 4.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                         VARIANT CONTINUES TO BE EXPRESSED IN SEVERAL TISSUES, EVEN AFTER
                                                                                                                                                                                                                       PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).
                                                                                                                                                                                                                                        EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
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FIBRONECTIN TYPE-III
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InterPro; IPR000087; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR003129; FN III.
InterPro; IPR003129; TSPN.
InterPro; IPR002035; VWFA.
Pfam; PF001391; Collagen; 4.
Pfam; PF00131; Collagen; 4.
Pfam; PF00210; TSPN; 1.
Pfam; PF000210; TSPN; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                               NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NC1).
TO CHOUDROITH SULFATE (POTENTIAL).
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TO CHOUNDOITH SULFATE (POTENTIAL).
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U-MAY-1991 (Rel. 18, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
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                                NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION (COL2)
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InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR002035; wWFA.
Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PF00092; wwa; 1.
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                                                        ISHIAWA N., NODAKA M., WEESEL R.A., Colten H.R.;
"Murine complement C2 and factor B genomic and cDNA cloning reveals
different mechanisms for multiple transcripts of C2 and B.";
J. Biol. Chem. 265:19040-19046[1990].
-I- FUNCTION: COMPONENT C2 WHICH IS PART OF THE CLASSICAL PATHWAY OF
THE COMPLEMENT SYSTEM IS CLEAVED BY ACTIVATED FACTOR C1 INTO TWO
FRAGMENTS: C2B AND C2A. C2A, A SERINE PROTEASE, THEN COMBINES WITH
COMPLEMENT FACTOR 48 TO GENERATE THE C3 OR C5 CONVERTASE.
-I- CATALYTIC ACTIVITY: CLEAVES C3 IN THE ALPHA-CHAIN TO YIELD C3A AND
C18AVAGES TAKE PLACE AT THE C-TERMINAL OF AN ARGININE RESIDUE.
-I- MISCELLANEOUS: C2 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
                                                                                                                                                                                                                                        PROTEIN.
-!- SIMILARITY: WITH COMPLEMENT FACTOR B.
-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) DOMAINS.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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EMBL; M60563; AAA37380.1; JOINED.
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M60577; AAA37381.1;
M60578; AAA37381.1;
M57891; AAA63294.1;
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                               SEQUENCE FROM N.A.
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23.2%; Pred. No. 0.003;
Ive 56; Mismatches 115; Indels
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COMPLEMENT C2B F
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SUSHI 2.
SUSHI 3.
PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00027; WWA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS50234; WFA; 1.
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16;

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Pfam; PF00092; vwa; 4.
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                                                                                                                                                                                                                                                            RADELINE SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

REAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

RA MEDLINE-9728851; PubMed-914349;

RA HGAGON D.L., Champliand M.F., Olsen B.R., Burgeson R.E.;

RA HGAGON D.L., Champliand M.F., Olsen B.R., Burgeson R.E.;

RA HGAGON D.L., Champliand M.F., Olsen B.R., Burgeson R.E.;

RA Complete primary structure of two splice variants of collagen (COL9A1), alpha 1(XI) collagen (COL12A1), alpha 1(XI)

RT chromosome 6912-q13.";

COCTARAINING FIBERILS, AND THE COL2AMIN TYPE I COLLAGEN-

COCTARAINING FIBERILS, AND THE COL2AMIN MAY BE

SURFACE OF THE FIBERILS, AND NO3 DOMAINS MAY BE

COCTARAINING FIBERILS, AND THE COL2AMIN HERD NO3

COCTARAINING FIBERILS, AND THE COL2AMIN HERD NO3

COCTARAINING FIBERILS, AND THE COL2AMIN HERD NO3

COCTARAINING FIBERILS, AND THE COLAGEN THE FINAL TISSUES

FORM CHAINS ON THE PERRONCES.

COCTARAINING TISSUES: BOTH

COCTARAINING TISSUES

COCTARAINING TISSUES: BOTH

COCTARAINING TISSUES

COCTARAINING TISSUES

COCTARAINING TISSUES

                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- PTM: GLYCGSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERROPTED HELICES (PACIT) FAMILY.
--- SIMILARITY: CONTAINS 4 VWFA DOMAINS.
--- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                 CAIC_HUMAN STANDARD; PRT; 3063 AA. 099715; 099716; 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000087; Collagen.
Interpro; IPR003961; FN_III.
Interpro; IPR003962; FNIII_repeat.
Interpro; IPR003129; TSPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U73778; AAC51244.1; -. EMBL; U73779; AAD40483.1; -.
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TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.

NOTHELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

HYDROXILATION (BY SIMILARITY).

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29.8%; Pred. No. 0.018;
ive 38; Mismatches 75; Indels 26
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TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
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MISSING (IN SHORT ISOFORM).
MW: 75FEA78FA8E48293 CRC64;
                                                                                                                                                        COLLAGEN ALPHA 1(XII) CHAIN FIBRONECTIN TYPE-III 1.
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FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 13.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
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FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
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FIBRONECTIN TYPE-III 7
FIBRONECTIN TYPE-III 7
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FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
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PRINTS; PRO0014; FNTYPEIII.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 17.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
PROSITE; PS50234; VWFA; 4.
Extracellular matrix; Connecti
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Matches 59; Conserv
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STRUCTURE BY NMR OF 1852-1885.
MEDLINE-92280705; PubMed=10350466;
Montserter R., Aubert-Foucher E., McLeish M.J., Hill J.M., Ficheux D., Jaquinod M., van der Rest M., Delage G., Penin F.;
"Structural analysis of the heparin-binding site of the NCl domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collagen XIV by CD and NMF. ...

Biochemistry 38:6479-6488(1999).

-!-FUNCTION: AN ADHESTVE ROLE BY INTEGRATING COLLAGEN BUNDLES. IT IS PROBABLY ASSOCIATED WITH THE SURFACE OF INTERSTITIAL COLLAGEN WHICH FIRST FROM THE FIREL MAD PROPREDES AS A RIGID ARM WHICH STICKS OUT FROM THE FIBRIL AND PROPREDES THE LARGE N-TERMINAL GLOBULAR DOWNIN INTO THE EXTRACELLULAR SPACE, WHERE IT MIGHT INTERACT WITH OTHER MATRIX MOLECULES OR CELL SURFACE
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                         440 DIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKFTK 499
                                                       72 DREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 127
                                                                       DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE
                                                                                                              128 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Embryo;
MEDLINE-93185668; PubMed-8444186;
Mealchli C., Trueb J., Kessler B., Winterhalter K.H., Trueb
"Complete primary structure of chicken collagen XIV.";
Eur. J. Blochem. 212:483-490(1993).
                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XIV) chain precursor (Undulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-9339443; PubMed=1339349;
Trueb J., Trueb B.;
"Type XIV collagen is a variant of undulin.";
Eur. J. Blochem. 207:549-557(1992).
                                                                                                                                                                                                                                                                       1888 AA.
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01-OCT-1996 (
01-MAR-2002 (
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TRIPLE-HELICAL REGION 2.
POLY-THR.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
CELL APPACIENT
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                                                                                                                                                                                                                                                                                                                    Primi; Pro0092; vwa: 2.
PRINTS; PRO0014; FINTYPEIII.
PRINTS; PRO00153; VWFADOMAIN.
SWART; SM00210; TSPN: 1.
SWART; SM00217; VWA: 2.
EXTRACCILLIAT MATIX; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
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CELL ATTACHMENT SITE (POTENTIAL).
W; 39915BB9F46DB973 CRC64;
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Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLLAGEN ALPHA 1(XIV) CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
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                                                                                                                   EMBL; X70793; CAA50064.1; -.
EMBL; X70792; CAA50063.1; -.
EMBL; X66138; CAA4628.1; -.
PIR; S22916; S22916.
PDB; 1B9P; 25-FEB-99.
PDB; 1B9P; 25-FEB-99.
INTERPOOF IPRO00967; COLLAGEN.
INTERPOOF IPRO03961; FN_III.
INTERPOOF IPRO03962; FNIII_repeat.
INTERPOOF IPRO03962; FNIII_repeat.
INTERPOOF IPRO03035; VWFA.
PFAM: PF01391; COLLAGEN.
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Pfam; PF02210; TSPN;
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                                                                                                                                                                                                                                         Eukaryota, Metazoa; Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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DR PIR; 542373; S42373

R HSSP, P02468; ITLE.

Mormpep; T20055.3; CE00478

InterPro; IPR0001851; BSF-like.

R InterPro; IPR000181; BSF-Like.

R InterPro; IPR000182; SEA.

R InterPro; IPR000181; SEA.

R InterPro; IPR00181; SEA.

R InterPro; IPR01818; SEA.

R InterPro; IPR
                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein T20G5.3 in chromosome III (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1 (PARTIAL).
EGF-LIKE 3.
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STRAIN-BRISTOL N2,
STRAIN-BRISTOL N2,
Berks M., Smith A.;
Berks M., Smith A.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: CONTAINS 45 EGF-LIKE DOMAINS.
-! SIMILARITY: CONTAINS 1 SEA DOMAINS.
-! SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-! SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-! CONTAINS 1 VWFA DOMAIN.
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Caenorhabditis elegans
                                   1267 NVYPCYRL 1274
   247 SVEDTYLL 254
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TENDENCY TOWARD DISTAL REGIONALIZATION. CONDENSING CARTILAGE SHOWS NO SIGNAL. FINALLY, AT THE LATE DIGIT STAGE, EXPRESSION BECOMES LARGELY RESTRICTED TO THE PERICHONDRIUM.

PTH: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT BACH END (BY SIMILARITY).

PTH: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-95246925; PubMed-7729585;
MEDLINE-95246925; PubMed-7729585;
Mei Y., Yang E.V., Klatt K.P., Tassava R.A.;
Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII collagen, a developmentally regulated extracellular matrix bev. Biol. 168:503-513(1994).

1- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-CONTAINING FIRBILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE SIBREACE OF THE FIBRILS, AND THE COLZ AND NC3 DOMAINS MAY BE LOCALIZED IN THE PERIFIGRILLAR MATRIX (BY SIMILARITY). COULD PLAY
                                                                                                                                                                                                                                                                                                                                                                                A DEVELOPMENTAL ROLE IN REGENERATION.
SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).
DEVELOPMENTAL STAGE: EXPRESSION STARTS AT 3 DAYS AFTER AMPUTATION IN CELLS OF THE BASAL LAYER OF THE WOUND EPITHELIUM. AT DAY 10, EXPRESSION IS FOUND IN BOTH THE BASAL WOUND EPITHELIUM. AT DAY 10, THE DISTAL MESENCHYME CELLS. AT MID-BUD AND LATE-BUD BLASTEMA STAGES, WOUND EPITHELIUM EXPRESSION HAS DECRREASED, WHEREAS THE MESENCHYME REMAINS STRONGLY ACTIVE IN TRANSCRIPTION AND SHOWED A
            --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 148
                                 602 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN
                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha [KXII] chain (Fragment).
Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                      149 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 203
                                                                   ::|| | ::| || |: || || || TRAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
--- SIMILARITY BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
--- SIMILARITY: CONTAINS 2 VWFA DOMAINS.
                                                                                                                                929 AA
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HSSP; P02751; IPNA.
InterPro; IPR003961; FN_III.
InterPro; IPR003035; VWFA.
Pfam; PF00041; fn3; 7.
Pfam; PF00092; VWA; 1.
SMART; SM00060; FN3; 5.
SWART; SM00327; VWA; 1.
PROSITE; PS50234; VWA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                            TENVCNSVKGPGGLNPPSNLVTSEPTPRSFRVTWVPPSQSVER----FKVEYYPVAGGRP 861
                                                                                                                                                                                                                                                                             18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage matrix protein.";
J. Biol. Chem. 265:19624-19631(1990).
-!- FUNCTION: CARTILAGE MATRIX PROTEIN IS A MAJOR COMPONENT OF THE EXTRACELLULAR MATRIX OF NONARTICULAR CARTILAGE. IT BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91060568; PubMed-2246248;
Jenkins R.N., Osborne-Lawrence S.L., Sinclair A.K., Eddy R.L. Jr.,
Byers M.G., Shows T.B., Duby A.D.;
"Structure and chromosomal location of the human gene encoding
                                                                                                                         FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Extracellular matrix; Connective tissue; Repeat; Cell adhesion; Collagen; Glycoprotein. Now_TER 1 1 ^{\rm 1}
                                                                                                                                                                                                                                  7.7%; Score 118; DB 1; Length 929; 21.2%; Pred. No. 0.047; ative 51; Mismatches 135; Indels
                                                                                                                                                                                                     MW; AE5D7485254FD954 CRC64;
                                                FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
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01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cartilage matrix protein precursor (Matrilin-1).
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                                       VWFA 1.
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231
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929 AA;
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P21941;
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Matches 57,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS--KDHVF 173
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''u: 2D880A8114C7940F CRC64;
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26.0%; Pred. No. 0.05;
iive 35; Mismatches
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EGF-LIKE.
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SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50234; VWFA; 2.
EGF-1ike domain; Signal; Glycoprotein
                                                                                                                                                                                                                                                                                                                  EMBL, M55682; AAB38702.1; --
EMBL, M55675; AAB38702.1; JOINED.
EMBL, M55676; AAB38702.1; JOINED.
EMBL, M55677; AAB38702.1; JOINED.
EMBL, M55679; AAB38702.1; JOINED.
EMBL, M55680; AAB38702.1; JOINED.
EMBL, M55681; AA7979.
INTERPROPOSITIONS.
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